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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/206,176*

CL

DATE: 03/23/94
TIME: 12:13:17

INPUT SET: S1765.raw

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: Garner, Ian
 6                       Dalrymple, Michael A
 7                       Prunkard, Donna E
 8                       Foster, Donald C
 9
10       (ii) TITLE OF INVENTION: Production of Fibrinogen in Transgenic
11             Animals
12
13      (iii) NUMBER OF SEQUENCES: 27
14
15       (iv) CORRESPONDENCE ADDRESS:
16             (A) ADDRESSEE: ZymoGenetics, Inc.
17             (B) STREET: 4225 Roosevelt Way, N.E.
18             (C) CITY: Seattle
19             (D) STATE: WA
20             (E) COUNTRY: USA
21             (F) ZIP: 98105
22
23        (v) COMPUTER READABLE FORM:
24             (A) MEDIUM TYPE: Floppy disk
25             (B) COMPUTER: IBM PC compatible
26             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29       (vi) CURRENT APPLICATION DATA:
30             (A) APPLICATION NUMBER:
31             (B) FILING DATE:
32             (C) CLASSIFICATION:
33
34     (viii) ATTORNEY/AGENT INFORMATION:
35             (A) NAME: Parker, Gary E
36             (B) REGISTRATION NUMBER: 31-648
37             (C) REFERENCE/DOCKET NUMBER: 93-15
38
39       (ix) TELECOMMUNICATION INFORMATION:
40             (A) TELEPHONE: 206-547-8080 ext 322
41             (B) TELEFAX: 206-548-2329
42
43
44
45    (2) INFORMATION FOR SEQ ID NO:1:
46
47        (i) SEQUENCE CHARACTERISTICS:
48             (A) LENGTH: 5943 base pairs
49             (B) TYPE: nucleic acid
50             (C) STRANDEDNESS: double
51             (D) TOPOLOGY: linear
```

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52
53          (ii) MOLECULE TYPE: DNA (genomic)
54
55
56        (vii) IMMEDIATE SOURCE:
57               (B) CLONE: Human Fibrinogen A-alpha chain
58
59         (ix) FEATURE:
60               (A) NAME/KEY: CDS
61               (B) LOCATION: join(31..84, 1154..1279, 1739..1922, 3055..3200,
62                   3786..5210)
63
64
65         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67   GTCTAGGAGC CAGCCCCACC CTTAGAAAAG ATG TTT TCC ATG AGG ATC GTC TGC        54
68                                     Met Phe Ser Met Arg Ile Val Cys
69                                      1                   5
70
71   CTA GTT CTA AGT GTG GTG GGC ACA GCA TGG GTATGGCCCT TTTCATTTTT          104
72   Leu Val Leu Ser Val Val Gly Thr Ala Trp
73      10                  15
74
75   TCTTCTTGCT TTCTCTCTGG TGTTTATTCC ACAAAGAGCC TGGAGGTCAG AGTCTACCTG      164
76
77   CTCTATGTCC TGACACACTC TTAGCTTTAT GACCCCAGGC CTGGGAGGAA ATTTCCTGGG      224
78
79   TGGGCTTGAC ACCTCAAGAA TACAGGGTAA TATGACACCA AGAGGAAGAT CTTAGATGGA      284
80
81   TGAGAGTGTA CAACTACAAG GGAAACTTTA GCATCTGTCA TTCAGTCTTA CCACATTTTG      344
82
83   TTTTGTTTTG TTTTAAAAAG GGCAAGAATT ATTTGCCATC CTTGTACCTA TAAAGCCTTG      404
84
85   GTGCATTATA ATGCTAGTTA ATGGAATAAA ACATTTTATG GTAAGATTTG TTTTCTTTAG      464
86
87   TTATTAATTT CTTGCTACTT GTCCATAATA AGCAGAACTT TTAGTGTTAG TACAGTTTTG      524
88
89   CTGAAAGGTT ATTGTTGTGT TTGTCAAGAC AGAAGAAAAA GCAAACGAAT TATCTTTGGA      584
90
91   AATATCTTTG CAGTATCAGA AGAGATTAGT TAGTAAGGCA ATACGCTTTT CCGCAGTAAT      644
92
93   GGTATTCTTT TAAATTATGA ATCCATCTCT AAAGGTTACA TAGAAACTTG AAGGAGAGAG      704
94
95   GAACATTCAG TTAAGATAGT CTAGGTTTTT CTACTGAAGC AGCAATTACA GGAGAAAGAG      764
96
97   CTCTACAGTA GTTTTCAACT TTCTGTCTGC AGTCATTAGT AAAAATGAAA AGGTAAAATT      824
98
99   TAACTGATTT TATAGATTCA AATAATTTTC CTTTTAGGAT GGATTCTTTA AAACTCCTAA      884
100
101  TATTTATCAA ATGCTTATTT AAGTGTCACA CACAGTTAAG AAATTTGTAC ACCTTGTCTC      944
102
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INPUT SET: S1765.raw

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103   CTTTAATTCT CATAACAACT CCATAAAATG GGTCCTAGGA TTTCCATTTG AAGATAAGAA      1004
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105   ACCTGAAGCT TGCCGAAGCC CTGTGTCTGC TCTCCTTAAT CTCTGTGAGA GTGCCATCTC      1064
106
107   TTCCTGGGGA CTTGTAGGCA TGCCACTGTC TCCTCTTCTG GCTAACATTG CTGTTGCTCT      1124
108
109   CTTTTGTGTA TGTGAATGAA TCTTTAAAG ACT GCA GAT AGT GGT GAA GGT GAC        1177
110                                      Thr Ala Asp Ser Gly Glu Gly Asp
111                                          20                  25
112
113   TTT CTA GCT GAA GGA GGA GGC GTG CGT GGC CCA AGG GTT GTG GAA AGA       1225
114   Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg
115           30              35                  40
116
117   CAT CAA TCT GCC TGC AAA GAT TCA GAC TGG CCC TTC TGC TCT GAT GAA       1273
118   His Gln Ser Ala Cys Lys Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu
119           45              50                  55
120
121   GAC TGG GTAAGCAGTC AGCGGGGGAA GCAGGAGATT CCTTCCCTCT GATGCTAGAG       1329
122   Asp Trp
123       60
124
125   GGGCTCACAG GCTGACCTGA TTGGTCCCAG AAACTTTTTT AAATAGAAAA TAATTGAATA      1389
126
127   GTTACCTACA TAGCAAATAA AGAAAAGGAA CCTACTCCCA AGAGCACTGT TTATTTACCT      1449
128
129   CCCCAACTCT GGATCATTAG TGGGTGAACA GACAGGATTT CAGTTGCATG CTCAGGCAAA      1509
130
131   ACCAGGCTCC TGAGTATTGT GGCCTCAATT TCCTGGCACC TATTTATGGC TAAGTGGACC      1569
132
133   CTCATTCCAG AGTTTCTCTG CGACCTCTAA CTAGTCCTCT TACCTACTTT TAAGCCAACT      1629
134
135   TATCTGGAAG AGAAAGGGTA GGAAGAAATG GGGGCTGCAT GGAAACATGC AAAATTATTC      1689
136
137   TGAATCTGAG AGATAGATCC TTACTGTAAT TTTCTCCCTT CACTTTCAG AAC TAC         1744
138                                                            Asn Tyr
139
140
141   AAA TGC CCT TCT GGC TGC AGG ATG AAA GGG TTG ATT GAT GAA GTC AAT       1792
142   Lys Cys Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn
143           65              70                  75
144
145   CAA GAT TTT ACA AAC AGA ATA AAT AAG CTC AAA AAT TCA CTA TTT GAA       1840
146   Gln Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu
147           80              85                  90
148
149   TAT CAG AAG AAC AAT AAG GAT TCT CAT TCG TTG ACC ACT AAT ATA ATG       1888
150   Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met
151   95                  100             105                 110
152
153   GAA ATT TTG AGA GGC GAT TTT TCC TCA GCC AAT  A GTAAGTATTA             1932
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INPUT SET: S1765.raw

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154   Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn
155                   115             120
156
157   CATATTTACT TCTTTGACTT TATAACAGAA ACAACAAAAA TCCTAAATAA ATATGATATC      1992
158
159   CGCTTATATC TATGACAATT TCATCCCAAA GTACTTAGTG TAGAAACACA TACCTTCATA      2052
160
161   ATATCCCTGA AAATTTTAAG AGGGAGCTTT TGTTTTCGTT ATTTTTTCAA AGTAAAAGAT      2112
162
163   GTTAACTGAG ATTGTTTAAG GTCACAAAAT AAGTCAGAAT TTTGGATTAA AACAAGAATT      2172
164
165   TAAATGTGTT CTTTTCAACA GTATATACTG AAAGTAGGAT GGGTCAGACT CTTTGAGTTG      2232
166
167   ATATTTTTGT TTCTGCTTTG TAAAGGTGAA AACTGAGAGG TCAAGGAACT TGTTCAAAGA      2292
168
169   CACAGAGCTG GGAATTCAAC TCCCAGACTC CACTGAGCTG ATTAGGTAGA TTTTTAAATT      2352
170
171   TAAAATATAG GGTCAAGCTA CGTCATTCTC ACAGTCTACT CATTAGGGTT AGGAAACATT      2412
172
173   GCATTCACTC TGGGCATGGA CAGCGAGTCT AGGGAGTCCT CAGTTTCTCA AGTTTTGCTT      2472
174
175   TGCCTTTTTA CACCTTCACA AACACTTGAC ATTTAAAATC AGTGATGCCA ACACTAGCTG      2532
176
177   GCAAGTGAGT GATCCTGTTG ACCCAAAACA GCTTAGGAAC CATTTCAAAT CTATAGAGTT      2592
178
179   AAAAAGAAAA GCTCATCAGT AAGAAAATCC AATATGTTCA AGTCCCTTGA TTAAGGATGT      2652
180
181   TATAAAATAA TTGAAATGCA ATCAAACCAA CTATTTTAAC TCCAAATTAC ACCTTTAAAA      2712
182
183   TTCCAAAGAA AGTTCTTCTT CTATATTTCT TTGGGATTAC TAATTGCTAT TAGGACATCT      2772
184
185   TAACTGGCAT TCATGGAAGG CTGCAGGGCA TAACATTATC CAAAAGTCAA ATGCCCCATA      2832
186
187   GGTTTTGAAC TCACAGATTA AACTGTAACC AAAATAAAAT TAGGCATATT TACAAGCTAG      2892
188
189   TTTCTTTCTT TCTTTTTTCT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT TTCTTTCTTT      2952
190
191   CTTTCTTTCT TTCTCCTTCC TTCCTTTCTT CCTTTCTTTT TTGCTGGCAA TTACAGACAA      3012
192
193   ATCACTCAGC AGCTACTTCA ATAACCATAT TTTCGATTTC AG   AC CGT GAT AAT       3065
194                                                    Asn Arg Asp Asn
195                                                                  125
196
197   ACC TAC AAC CGA GTG TCA GAG GAT CTG AGA AGC AGA ATT GAA GTC CTG       3113
198   Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu
199                   130             135             140
200
201   AAG CGC AAA GTC ATA GAA AAA GTA CAG CAT ATC CAG CTT CTG CAG AAA       3161
202   Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys
203                   145             150             155
204
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INPUT SET: S1765.raw

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205  AAT GTT AGA GCT CAG TTG GTT GAT ATG AAA CGA CTG GAG GTAAGTATGT        3210
206  Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu Glu
207          160                 165                 170
208
209  GGCTGTGGTC CCGAGTGTCC TTGTTTTTGA GTAGAGGGAA AAGGAAGGCG ATAGTTATGC     3270
210
211  ACTGAGTGTC TACTATATGC AGAGAAAAGT GTTATATCCA TCATCTACCT AAAAGTAGGT     3330
212
213  ATTATTTTCC TCACTCCACA GTTGAAGAAA AAAAAATTCA GAGATATTAA GTAAATTTTC     3390
214
215  CAACGTACAT AGATAGTAAT TCAAAGCAAT GTTCAGTCCC TGTCTATTCC AAGCCATTAC     3450
216
217  ATCACCACAC CTCTGAGCCC TCAGCCTGAG TTCACCAAGG ATCATTTAAT TAGCGTTTCC     3510
218
219  TTTGAGAGGG AATAGCACCT TACTCTTGAT CCATTCTGAG GCTAAGATGA ATTAAACAGC     3570
220
221  ATCCATTGCT TATCCTGGCT AGCCCTGCAA TACCCAACAT CTCTTCCACT GAGGGTGCTC     3630
222
223  GATAGGCAGA AAACAGAGAA TATTAAGTGG TAGGTCTCCG AGTCAAAAAA AATGAAACCA     3690
224
225  GTTTCCAGAA GGAAAATTAA CTACCAGGAA CTCAATAGAC GTAGTTTATG TATTTGTATC     3750
226
227  TACATTTTCT CTTTATTTTT CTCCCCTCTC TCTAG GTG GAC ATT GAT ATT AAG       3803
228                                          Val Asp Ile Asp Ile Lys
229                                                          175
230
231  ATC CGA TCT TGT CGA GGG TCA TGC AGT AGG GCT TTA GCT CGT GAA GTA       3851
232  Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val
233          180                 185                 190
234
235  GAT CTG AAG GAC TAT GAA GAT CAG CAG AAG CAA CTT GAA CAG GTC ATT       3899
236  Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys Gln Leu Glu Gln Val Ile
237          195                 200                 205
238
239  GCC AAA GAC TTA CTT CCC TCT AGA GAT AGG CAA CAC TTA CCA CTG ATA       3947
240  Ala Lys Asp Leu Leu Pro Ser Arg Asp Arg Gln His Leu Pro Leu Ile
241          210                 215                 220
242
243  AAA ATG AAA CCA GTT CCA GAC TTG GTT CCC GGA AAT TTT AAG AGC CAG       3995
244  Lys Met Lys Pro Val Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln
245  225                 230                 235                 240
246
247  CTT CAG AAG GTA CCC CCA GAG TGG AAG GCA TTA ACA GAC ATG CCG CAG       4043
248  Leu Gln Lys Val Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln
249          245                 250                 255
250
251  ATG AGA ATG GAG TTA GAG AGA CCT GGT GGA AAT GAG ATT ACT CGA GGA       4091
252  Met Arg Met Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly
253          260                 265                 270
254
255  GGC TCC ACC TCT TAT GGA ACC GGA TCA GAG ACG GAA AGC CCC AGG AAC       4139
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INPUT SET: S1765.raw

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256   Gly Ser Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn
257           275             280             285
258
259   CCT AGC AGT GCT GGA AGC TGG AAC TCT GGG AGC TCT GGA CCT GGA AGT      4187
260   Pro Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser
261           290             295             300
262
263   ACT GGA AAC CGA AAC CCT GGG AGC TCT GGG ACT GGA GGG ACT GCA ACC      4235
264   Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala Thr
265   305             310             315             320
266
267   TGG AAA CCT GGG AGC TCT GGA CCT GGA AGT GCT GGA AGC TGG AAC TCT      4283
268   Trp Lys Pro Gly Ser Ser Gly Pro Gly Ser Ala Gly Ser Trp Asn Ser
269           325             330             335
270
271   GGG AGC TCT GGA ACT GGA AGT ACT GGA AAC CAA AAC CCT GGG AGC CCT      4331
272   Gly Ser Ser Gly Thr Gly Ser Thr Gly Asn Gln Asn Pro Gly Ser Pro
273           340             345             350
274
275   AGA CCT GGT AGT ACC GGA ACC TGG AAT CCT GGC AGC TCT GAA CGC GGA      4379
276   Arg Pro Gly Ser Thr Gly Thr Trp Asn Pro Gly Ser Ser Glu Arg Gly
277           355             360             365
278
279   AGT GCT GGG CAC TGG ACC TCT GAG AGC TCT GTA TCT GGT AGT ACT GGA      4427
280   Ser Ala Gly His Trp Thr Ser Glu Ser Ser Val Ser Gly Ser Thr Gly
281           370             375             380
282
283   CAA TGG CAC TCT GAA TCT GGA AGT TTT AGG CCA GAT AGC CCA GGC TCT      4475
284   Gln Trp His Ser Glu Ser Gly Ser Phe Arg Pro Asp Ser Pro Gly Ser
285   385             390             395             400
286
287   GGG AAC GCG AGG CCT AAC AAC CCA GAC TGG GGC ACA TTT GAA GAG GTG      4523
288   Gly Asn Ala Arg Pro Asn Asn Pro Asp Trp Gly Thr Phe Glu Glu Val
289               405             410             415
290
291   TCA GGA AAT GTA AGT CCA GGG ACA AGG AGA GAG TAC CAC ACA GAA AAA      4571
292   Ser Gly Asn Val Ser Pro Gly Thr Arg Arg Glu Tyr His Thr Glu Lys
293               420             425             430
294
295   CTG GTC ACT TCT AAA GGA GAT AAA GAG CTC AGG ACT GGT AAA GAG AAG      4619
296   Leu Val Thr Ser Lys Gly Asp Lys Glu Leu Arg Thr Gly Lys Glu Lys
297           435             440             445
298
299   GTC ACC TCT GGT AGC ACA ACC ACC ACG CGT CGT TCA TGC TCT AAA ACC      4667
300   Val Thr Ser Gly Ser Thr Thr Thr Thr Arg Arg Ser Cys Ser Lys Thr
301           450             455             460
302
303   GTT ACT AAG ACT GTT ATT GGT CCT GAT GGT CAC AAA GAA GTT ACC AAA      4715
304   Val Thr Lys Thr Val Ile Gly Pro Asp Gly His Lys Glu Val Thr Lys
305   465             470             475             480
306
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307   GAA GTG GTG ACC TCC GAA GAT GGT TCT GAC TGT CCC GAG GCA ATG GAT        4763
308   Glu Val Val Thr Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp
309               485                 490                 495
310
311   TTA GGC ACA TTG TCT GGC ATA GGT ACT CTG GAT GGG TTC CGC CAT AGG        4811
312   Leu Gly Thr Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg
313               500                 505                 510
314
315   CAC CCT GAT GAA GCT GCC TTC TTC GAC ACT GCC TCA ACT GGA AAA ACA        4859
316   His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr
317               515                 520                 525
318
319   TTC CCA GGT TTC TTC TCA CCT ATG TTA GGA GAG TTT GTC AGT GAG ACT        4907
320   Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr
321           530                 535                 540
322
323   GAG TCT AGG GGC TCA GAA TCT GGC ATC TTC ACA AAT ACA AAG GAA TCC        4955
324   Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu Ser
325   545                 550                 555                 560
326
327   AGT TCT CAT CAC CCT GGG ATA GCT GAA TTC CCT TCC CGT GGT AAA TCT        5003
328   Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly Lys Ser
329               565                 570                 575
330
331   TCA AGT TAC AGC AAA CAA TTT ACT AGT AGC ACG AGT TAC AAC AGA GGA        5051
332   Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr Asn Arg Gly
333               580                 585                 590
334
335   GAC TCC ACA TTT GAA AGC AAG AGC TAT AAA ATG GCA GAT GAG GCC GGA        5099
336   Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala Asp Glu Ala Gly
337               595                 600                 605
338
339   AGT GAA GCC GAT CAT GAA GGA ACA CAT AGC ACC AAG AGA GGC CAT GCT        5147
340   Ser Glu Ala Asp His Glu Gly Thr His Ser Thr Lys Arg Gly His Ala
341           610                 615                 620
342
343   AAA TCT CGC CCT GTC AGA GGT ATC CAC ACT TCT CCT TTG GGG AAG CCT        5195
344   Lys Ser Arg Pro Val Arg Gly Ile His Thr Ser Pro Leu Gly Lys Pro
345   625                 630                 635                 640
346
347   TCC CTG TCC CCC TAGACTAAGT TAAATATTTC TGCACAGTGT TCCCATGGCC           5247
348   Ser Leu Ser Pro
349                   645
350
351   CCTTGCATTT CCTTCTTAAC TCTCTGTTAC ACGTCATTGA AACTACACTT TTTTGGTCTG     5307
352
353   TTTTTGTGCT AGACTGTAAG TTCCTTGGGG GCAGGGCCTT TGTCTGTCTC ATCTCTGTAT     5367
354
355   TCCCAAATGC CTAACAGTAC AGAGCCATGA CTCAATAAAT ACATGTTAAA TGGATGAATG     5427
356
357   AATTCCTCTG AAACTCTATT TGAGCTTATT TAGTCAAATT CTTTCACTAT TCAAAGTGTG     5487
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358
359   TGCTATTAGA ATTGTCACCC AACTGATTAA TCACATTTTT AGTATGTGTC TCAGTTGACA      5547
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361   TTTAGGTCAG GCTAAATACA AGTTGTGTTA GTATTAAGTG AGCTTAGCTA CCTGTACTGG      5607
362
363   TTACTTGCTA TTAGTTTGTG CAAGTAAAAT TCCAAATACA TTTGAGGAAA ATCCCCTTTG      5667
364
365   CAATTTGTAG GTATAAATAA CCGCTTATTT GCATAAGTTC TATCCCACTG TAAGTGCATC      5727
366
367   CTTTCCCTAT GGAGGGAAGG AAAGGAGGAA GAAAGAAAGG AAGGGAAAGA AACAGTATTT      5787
368
369   GCCTTATTTA ATCTGAGCCG TGCCTATCTT TGTAAAGTTA AATGAGAATA ACTTCTTCCA      5847
370
371   ACCAGCTTAA TTTTTTTTTT AGACTGTGAT GATGTCCTCC AAACACATCC TTCAGGTACC      5907
372
373   CAAAGTGGCA TTTTCAATAT CAAGCTATCC GGATCC                                5943
374
375
376   (2) INFORMATION FOR SEQ ID NO:2:
377
378          (i) SEQUENCE CHARACTERISTICS:
379              (A) LENGTH: 644 amino acids
380              (B) TYPE: amino acid
381              (D) TOPOLOGY: linear
382
383         (ii) MOLECULE TYPE: protein
384
385         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
386
387   Met Phe Ser Met Arg Ile Val Cys Leu Val Leu Ser Val Val Gly Thr
388    1               5                  10                  15
389
390   Ala Trp Thr Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly
391                20                  25                  30
392
393   Gly Val Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys
394                35                  40                  45
395
396   Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
397        50                  55                  60
398
399   Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln Asp
400    65                  70                  75                  80
401
402   Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu Tyr Gln
403                85                  90                  95
404
405   Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met Glu Ile
406                100                 105                 110
407
408   Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp Asn Thr Tyr Asn
```

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409              115                  120                  125
410
411    Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu Lys Arg Lys
412        130                  135                  140
413
414    Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys Asn Val Arg
415    145                  150                  155                  160
416
417    Ala Gln Leu Val Asp Met Lys Arg Leu Glu Val Asp Ile Asp Ile Lys
418                    165                  170                  175
419
420    Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val
421            .   180                  185          .       190
422
423    Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys Gln Leu Glu Gln Val Ile
424        195              .       200                  205
425
426    Ala Lys Asp Leu Leu Pro Ser Arg Asp Arg Gln His Leu Pro Leu Ile
427        210                  215                  220
428
429    Lys Met Lys Pro Val Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln
430    225                  230                  235                  240
431
432    Leu Gln Lys Val Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln
433                245                  250                  255
434
435    Met Arg Met Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly
436            260                  265                  270
437
438    Gly Ser Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn
439        275                  280                  285
440
441    Pro Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser
442        290                  295                  300
443
444    Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala Thr
445    305                  310                  315                  320
446
447    Trp Lys Pro Gly Ser Ser Gly Pro Gly Ser Ala Gly Ser Trp Asn Ser
448                325                  330                  335
449
450    Gly Ser Ser Gly Thr Gly Ser Thr Gly Asn Gln Asn Pro Gly Ser Pro
451                340                  345                  350
452
453    Arg Pro Gly Ser Thr Gly Thr Trp Asn Pro Gly Ser Ser Glu Arg Gly
454        355                  360                  365
455
456    Ser Ala Gly His Trp Thr Ser Glu Ser Ser Val Ser Gly Ser Thr Gly
457        370                  375                  380
458
459    Gln Trp His Ser Glu Ser Gly Ser Phe Arg Pro Asp Ser Pro Gly Ser
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460   385                      390                      395                      400
461
462   Gly Asn Ala Arg Pro Asn Asn Pro Asp Trp Gly Thr Phe Glu Glu Val
463               405                      410                      415
464
465   Ser Gly Asn Val Ser Pro Gly Thr Arg Arg Glu Tyr His Thr Glu Lys
466               420                      425                      430
467
468   Leu Val Thr Ser Lys Gly Asp Lys Glu Leu Arg Thr Gly Lys Glu Lys
469           435                      440                      445
470
471   Val Thr Ser Gly Ser Thr Thr Thr Thr Arg Arg Ser Cys Ser Lys Thr
472           450                      455                      460
473
474   Val Thr Lys Thr Val Ile Gly Pro Asp Gly His Lys Glu Val Thr Lys
475   465                      470                      475                      480
476
477   Glu Val Val Thr Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp
478               485                      490                      495
479
480   Leu Gly Thr Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg
481           500                      505                      510
482
483   His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr
484           515                      520                      525
485
486   Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr
487           530                      535                      540
488
489   Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu Ser
490   545                      550                      555                      560
491
492   Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly Lys Ser
493               565                      570                      575
494
495   Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr Asn Arg Gly
496           580                      585                      590
497
498   Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala Asp Glu Ala Gly
499           595                      600                      605
500
501   Ser Glu Ala Asp His Glu Gly Thr His Ser Thr Lys Arg Gly His Ala
502           610                      615                      620
503
504   Lys Ser Arg Pro Val Arg Gly Ile His Thr Ser Pro Leu Gly Lys Pro
505   625                      630                      635                      640
506
507   Ser Leu Ser Pro
508
509
510   (2) INFORMATION FOR SEQ ID NO:3:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/206,176*

DATE: 03/23/94
TIME: 12:14:12

INPUT SET: S1765.raw

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511
512          (i)  SEQUENCE CHARACTERISTICS:
513               (A)  LENGTH: 8878 base pairs
514               (B)  TYPE: nucleic acid
515               (C)  STRANDEDNESS: double
516               (D)  TOPOLOGY: linear
517
518         (ii)  MOLECULE TYPE: DNA (genomic)
519
520
521        (vii)  IMMEDIATE SOURCE:
522               (B)  CLONE: human fibrinogen B-beta chain
523
524         (ix)  FEATURE:
525               (A)  NAME/KEY: misc_RNA
526               (B)  LOCATION: 1..469
527
528         (ix)  FEATURE:
529               (A)  NAME/KEY: exon
530               (B)  LOCATION: 470..583
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532         (ix)  FEATURE:
533               (A)  NAME/KEY: intron
534               (B)  LOCATION: 584..3257
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536         (ix)  FEATURE:
537               (A)  NAME/KEY: exon
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540         (ix)  FEATURE:
541               (A)  NAME/KEY: intron
542               (B)  LOCATION: 3450..3938
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544         (ix)  FEATURE:
545               (A)  NAME/KEY: exon
546               (B)  LOCATION: 3939..4122
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550               (B)  LOCATION: 4123..5042
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554               (B)  LOCATION: 5043..5270
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556         (ix)  FEATURE:
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560         (ix)  FEATURE:
561               (A)  NAME/KEY: exon
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562                    (B) LOCATION: 5831..5944
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564        (ix) FEATURE:
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568        (ix) FEATURE:
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570                    (B) LOCATION: 6633..6758
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572        (ix) FEATURE:
573                    (A) NAME/KEY: intron
574                    (B) LOCATION: 6759..6966
575
576        (ix) FEATURE:
577                    (A) NAME/KEY: exon
578                    (B) LOCATION: 6967..7252
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580        (ix) FEATURE:
581                    (A) NAME/KEY: intron
582                    (B) LOCATION: 7253..7870
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584
585        (ix) FEATURE:
586                    (A) NAME/KEY: exon
587                    (B) LOCATION: 7871..8102
588
589        (ix) FEATURE:
590                    (A) NAME/KEY: 3'UTR
591                    (B) LOCATION: 8103..8537
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593        (ix) FEATURE:
594                    (A) NAME/KEY: misc_RNA
595                    (B) LOCATION: 8538..8878
596
597        (ix) FEATURE:
598                    (A) NAME/KEY: CDS
599                    (B) LOCATION: join(470..583, 3258..3449, 3939..4122, 5043..5270,
600                          5831..5944, 6633..6758, 6967..7252, 7871..8102)
601
602
603        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
604
605   GAATTCATGC CCCTTTTGAA ATAGACTTAT GTCATTGTCA GAAAACATAA GCATTTATGG        60
606
607   TATATCATTA ATGAGTCACG ATTTTAGTGG TTGCCTTGTG AGTAGGTCAA ATTTACTAAG       120
608
609   CTTAGATTTG TTTTCTCACA TATTCTTTCG GAGCTTGTGT AGTTTCCACA TTAATTTACC       180
610
611   AGAAACAAGA TACACACTCT CTTTGAGGAG TGCCCTAACT TCCCATCATT TTGTCCAATT       240
612
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613  AAATGAATTG AAGAAATTTA ATGTTTCTAA ACTAGACCAA CAAAGAATAA TAGTTGTATG    300
614
615  ACAAGTAAAT AAGCTTTGCT GGGAAGATGT TGCTTAAATG ATAAAATGGT TCAGCCAACA    360
616
617  AGTGAACCAA AAATTAAATA TTAACTAAGG AAAGGTAACC ATTTCTGAAG TCATTCCTAG    420
618
619  CAGAGGACTC AGATATATAT AGGATTGAAG ATCTCTCAGT TAAGTCTAC ATG AAA        475
620                                                         Met Lys
621                                                          1
622
623  AGG ATG GTT TCT TGG AGC TTC CAC AAA CTT AAA ACC ATG AAA CAT CTA     523
624  Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys His Leu
625          5               10              15
626
627  TTA TTG CTA CTA TTG TGT GTT TTT CTA GTT AAG TCC CAA GGT GTC AAC     571
628  Leu Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly Val Asn
629          20              25              30
630
631  GAC AAT GAG GAG GTGAATTTTT TAAAGCATTA TTATATTATT AGTAGTATTA         623
632  Asp Asn Glu Glu
633   35
634
635  TTAATATAAG ATGTAACATA ATCATATTAT GTGCTTATTT TAATGAAATT AGCATTGCTT    683
636
637  ATAGTTATGA AATGGAATTG TTAACCTCTG ACTTATTGTA TTTAAAGAAT GTTTCATAGT    743
638
639  ATTTCTTATA TAAAAACAAA GTAATTTCTT GTTTTCTAGT TTATCACCTT TGTTTTCTTA    803
640
641  AGATGAGGAT GGCTTAGCTA ATGTAAGATG TGTTTTTCTC ACTTGCTATT CTGAGTACTG    863
642
643  TGATTTTCAT TTACTTCTAG CAATACAGGA TTACAATTAA GAGGACAAGA TCTGAAAATC    923
644
645  TCACAAACTA TAAAATAATA AAAGAGCAGA ATTTTAAGAT AAAAGAAACT GGTGGTAGGT    983
646
647  AGATTGTTCT TTGGTGAAGG AAGGTAATAT ATATTGTTAC TGAGATTACT ATTTATAAAA   1043
648
649  ATTATAACTA AGCCTAAAAG CAAAATACAT CAAGTGTAAT GATAGAAAAT GAAATATTGC   1103
650
651  TTTTTTCAGA TGAAAGTTC AAATTAGAGT TAGTGTGTAT TGTTATTATT AATAGTTATG    1163
652
653  AAACACGGTT CAGTCTAATT TATTTATTTG TAGAACAGTT TGTCCTCAAC TATTATTTTT   1223
654
655  GCTGACTTAT TGCTGTTAAT TTGCAGTTAC TAAAAATACA GAAATGCATT TAGGACAATG   1283
656
657  GATATTTAAG AAATTTAAAT TTTATCATCA AACGTATCAT GGCCAAATTT CTTACATATA   1343
658
659  GCATAGTATC ATTAAACTAG AAATAAGAAT ACACAATAAT ATTTAAATGA AGTGATTCAT   1403
660
661  TTCGGATCAT TATTGAGTTT CAAGGGAACT TGAGTGTTGT ACTTATCAGA CTCTACATGT   1463
662
663  AAGAACATAT AGTTAATCTG GTTGTGTGTG TAAAAACATA TGGTTAATCT GGTTAAGTCT   1523
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664
665   GGTTAATCAT ATTAGGTAAG AAAAATGTAA AGAATGTGTA AGACGAAATT TTTGTAAAGT   1583
666
667   ACTCTGCAAA GCACTTTCAC ATTTCTGCTT ATCAACTAAA CCTCACAGAG ATAGTTTAAT   1643
668
669   AGTTTAGGCT TTAAAATGGA TTTTGATTAT TCAACAAGTG GCCTTCATAA TTTCTTTAAG   1703
670
671   TGTTTTTCTT TAAGTATATA CTTTCTTTAA ATATTTTTTA AAATTTCCTT TTCTCTAGTA   1763
672
673   AAGCCAGACC ATCCATGCTA CCTCTCTAGT GGCACTCTGA AATAAAAAGA AAATAGTTTT   1823
674
675   CTCTGTTATA ATTGTATTTG TAATAAGCAG ATGAATCACA TTTCTTAAAA TTTGTTTTAG   1883
676
677   AGAGGGTAAG CTCTGACTAG GACCATGACT TCAATGTGAA ATATGTATAT ATCCTCCGAA   1943
678
679   TCTTTACATA TTAAGAATGT ATATAGTCAA CTGGTTAAAC AGGAAAATCT GGAACAGCCT   2003
680
681   GGCTGGGTTT TAATCTTAGC ACCATCCTAC TAAATGTTAA ATAATATTAT AATCTAATGA   2063
682
683   ATAAATGACA ATGCAATTCC AAATAGAGTT CATCTGATGA CTTCTAGACT CACAAAATTG   2123
684
685   CAAGAGAGCT CAGTTGTTGC TCAGTTGTTC CAAATCATGT CGTTTGTTAA TTTGTAATTA   2183
686
687   AGCTCCAAAG GATGTATAGC TACTGACAAA AAAAAAAATG AGAATGTAGT TAATCCAAAT   2243
688
689   CAAAACTTTC CTATTGCAAT GCGTATTTTC TGCTTCATTA TCCTTTAATA TAATATTTTA   2303
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691   AGTTAGCAAG TAATTTTAAT TACAATGCAC AAGCCTTGAG AATTATTTTA AATATAAGAA   2363
692
693   AATCATAATG TTTGATAAAG AAATCATGTA AGAAATTTCA AGATAATGGT TTAACAAATA   2423
694
695   ATTTTGTTGA TAGAAGATAA GACTAAAAGT GAAATTCGAA GTGGAGAGGA CACTTAAACT   2483
696
697   GTAGTACTTG TTATGTGTGA TTCCAGTAAA AATAGTAATG AGCACTTATT ATTGCCAAGT   2543
698
699   ACTGTTCTGA GGGTACCATA TGCAATAAGT TATTTAATCC TTACAATAAT CTTGTAAGGC   2603
700
701   AGATTCAAAC TATCATTACA CTTATTTTAC AGATGAGAAA ACTGGGGCAC AGATAAAGCA   2663
702
703   ACTTGCCCAA GGTCTCATAG CTGTAAGTCA ACCCTACGGT CAAGACCTAC AAGTAGCCGA   2723
704
705   GCTCCAGAGT ACATTATGAG GGTCAAAGAT TGTCTTATTA CAAATAAATT CCAAGTAGAA   2783
706
707   TCAACCTTTA ATAAGTCTTT AATGTCTCTT AAATATGTTT ATATAGGAGT CTAATCACCA   2843
708
709   ATTCACAAAA ATGAAAGTAG GGAAATGATT AACAATAATC ATAGGAATCT AACAATCCAA   2903
710
711   GTGGCTTGAG AATATTCATT CTTCTTGACA GTATAGATTC TTTACAATTT CGTAAGTTCC   2963
712
713   AATGTATGTT TTAGGAATAT GAGGTCATTA CTATTCATAA TCTGATACAG CTTTATCCTA   3023
714
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715    AGGCCTCTCT TTAAAAACTA CACTGCATCA TAGCTTTTTT GTGCAGTTGG TCTTTCTACT    3083
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717    GTTACTGAAC AGTAAGCAAC CTACAGATTC ACTATCACCA ACCAGCCAGT TGATGGATCT    3143
718
719    TAAGCAAATT ATCAAGCTTG TGATAACCTA AATTATAAAA TGAGGGTGTT GGAATAGTTA    3203
720
721    CATTCCAAAT CTTCTATAAC ACTCTGTATT ATATTTCTGC CTCATTCCTT GTAG GGT       3260
722                                                                   Gly
723
724
725    TTC TTC AGT GCC CGT GGT CAT CGA CCC CTT GAC AAG AAG AGA GAA GAG     3308
726    Phe Phe Ser Ala Arg Gly His Arg Pro Leu Asp Lys Lys Arg Glu Glu
727     40              45                  50                  55
728
729    GCT CCC AGC CTG AGG CCT GCC CCA CCG CCC ATC AGT GGA GGT GGC TAT     3356
730    Ala Pro Ser Leu Arg Pro Ala Pro Pro Pro Ile Ser Gly Gly Gly Tyr
731                     60                  65                  70
732
733    CGG GCT CGT CCA GCC AAA GCA GCT GCC ACT CAA AAG AAA GTA GAA AGA     3404
734    Arg Ala Arg Pro Ala Lys Ala Ala Ala Thr Gln Lys Lys Val Glu Arg
735                     75                  80                  85
736
737    AAA GCC CCT GAT GCT GGA GGC TGT CTT CAC GCT GAC CCA GAC CTG         3449
738    Lys Ala Pro Asp Ala Gly Gly Cys Leu His Ala Asp Pro Asp Leu
739             90                  95                  100
740
741    GTGGGTGCAC TGATGTTTCT TGCAGTGGTG GCTCTCTCAT GCAGAGAAAG CCTGTAGTCA    3509
742
743    TGGCAGTCTG CTAATGTTTC ACTGACCCAC ATTACCATCA CTGTTATTTT GTTTGTTTAT    3569
744
745    TTTGGAAATA AAATTCAAAA CATAAACATA TTGGGCCTTT GGTTTAGGCT TTCTTTCTTG    3629
746
747    TTTTCTTTGG TCTGGGCCCA AAATTTCAAA TTAGGATATG TGGGTGCCAC CTTTCCATTT    3689
748
749    GTATTTTGCC ACTGCCTTTG TTTAGTTGGT AAAATTTTCA TAGCCCAATT ATATTTTTTC    3749
750
751    TGGGGTAAGT AATATTTTAA ATCTCTATGA GAGTATGATG ATGACTTTCG AATTTCTGGT    3809
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753    CTTACAGAAA ACCAAATAAT AAATTTTTAT GTTGGCTAAT CGTATCGCTG AATTTTCCTA    3869
754
755    TGTGCTATTT TAACAAATGT CCATGACCCA AATCCTTCAT CTAATGCCTG CTATTTTCTT    3929
756
757    TGTTTTTAG GGG GTG TTG TGT CCT ACA GGA TGT CAG TTG CAA GAG GCT       3977
758             Gly Val Leu Cys Pro Thr Gly Cys Gln Leu Gln Glu Ala
759             105                 110                 115
760
761    TTG CTA CAA CAG GAA AGG CCA ATC AGA AAT AGT GTT GAT GAG TTA AAT     4025
762    Leu Leu Gln Gln Glu Arg Pro Ile Arg Asn Ser Val Asp Glu Leu Asn
763             120                 125                 130
764
765    AAC AAT GTG GAA GCT GTT TCC CAG ACC TCC TCT TCT TCC TTT CAG TAC     4073
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766   Asn Asn Val Glu Ala Val Ser Gln Thr Ser Ser Ser Ser Phe Gln Tyr
767           135                 140                 145
768
769   ATG TAT TTG CTG AAA GAC CTG TGG CAA AAG AGG CAG AAG CAA GTA AAA   G   4122
770   Met Tyr Leu Leu Lys Asp Leu Trp Gln Lys Arg Gln Lys Gln Val Lys
771           150                 155                 160
772
773   GTAGATATCC TTGTGCTTTC CATTCGATTT TCAGCTATAA AATTGGAACC GTTAGACTGC        4182
774
775   CACGAGAATG CATGGTTGTG AGAAGATTAA CATTTCTGGG TTAGTGAATA GCATTCATAC        4242
776
777   GCTTTTGGGC ACCTTCCCCT GCAACTTGCC AGATAAGCAC TATTCAGCTC TTATTCCCAG        4302
778
779   TCTGACATCA GCAAGTGTGA TTTTCTATGA AAAATTCTAC TATGACTCCT TATTTTAAGT        4362
780
781   ATACAAGAAA CTTGTGACTC AGAAGATAAT ATTTACAGAG TGGAAAAAAA CCCCTAGCAT        4422
782
783   TTATAGTTTT AACATTTGAG GTTTTGAATG AGAGAGTTAT CCATAATATA TTCAATTGTG        4482
784
785   TTGTGGATAA TGACACCTAA CCTGTGAATC TTGAGGTCAG AATGTTGAGT GCTGTTGACT        4542
786
787   TGGTGGTCAG GAAACAGCTA GTGCGTGAGC CTGGCACAGG CATCTCAGTG AGTAGCATAC        4602
788
789   CCACAGTTGG AAATTTTTCA AAGAAATCAA AGGAATCATG ACATCTTATA AATTTCAAGG        4662
790
791   TTCTGCTATA CTTATGTGAA ATGGATAAAT AAATCAAGCA TATCCACTCT GTAAGATTGA        4722
792
793   ACTTCTCAGA TGGAAGACCC CAATACTGCT TTCTCCTCTT TTCCCTCACC AAAGAAATAA        4782
794
795   ACAACCTATT TCATTTATTA CTGGACACAA TCTTTAGCGT ATACCTATGG TAAATTACTA        4842
796
797   GTATGGTGGT TAGGATTTAT GTTAATTTGT ATATGTCATG CGCCAAATCA TTTCCACTAA        4902
798
799   ATATGACTAT ATATCATAAC TGCTTGGTGA TAGCTCAGTG TTTAATAGTT TATTCTCAGA        4962
800
801   AAATCAAAAT TGTATAGTTA AATACATTAG TTTTATGAGG CAAAAATGCT AACTATTTCT        5022
802
803   ACATAATTTC ATTTTTCCAG   AT AAT GAA AAT GTA GTC AAT GAG TAC TCC            5071
804                         Asp Asn Glu Asn Val Val Asn Glu Tyr Ser
805                             165                 170
806
807   TCA GAA CTG GAA AAG CAC CAA TTA TAT ATA GAT GAG ACT GTG AAT AGC        5119
808   Ser Glu Leu Glu Lys His Gln Leu Tyr Ile Asp Glu Thr Val Asn Ser
809       175                 180                 185
810
811   AAT ATC CCA ACT AAC CTT CGT GTG CTT CGT TCA ATC CTG GAA AAC CTG        5167
812   Asn Ile Pro Thr Asn Leu Arg Val Leu Arg Ser Ile Leu Glu Asn Leu
813   190                 195                 200                 205
814
815   AGA AGC AAA ATA CAA AAG TTA GAA TCT GAT GTC TCA GCT CAA ATG GAA        5215
816   Arg Ser Lys Ile Gln Lys Leu Glu Ser Asp Val Ser Ala Gln Met Glu
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INPUT SET: S1765.raw

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817                210                 215                 220
818
819   TAT TGT CGC ACC CCA TGC ACT GTC AGT TGC AAT ATT CCT GTG GTG TCT          5263
820   Tyr Cys Arg Thr Pro Cys Thr Val Ser Cys Asn Ile Pro Val Val Ser
821            225                 230                 235
822
823   GGC AAA  G GTAACTGATT CATAAACATA TTTTTAGAGA GTTCCAGAAG AACTCACACA          5320
824   Gly Lys
825
826
827   CCAAAAATAA GAGAACAACA ACAACAACAA AAATGCTAAG TGGATTTTCC CAACAGATCA          5380
828
829   TAATGACATT ACAGTACATC ATAAAAATAT CCTTAGCCAG TTGTGTTTTG GACTGGCCTG          5440
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831   GTGCATTTGC TGGTTTTGAT GAGCAGGATG GGGCACAGGT AGTCCCAGGG GTGGCTGATG          5500
832
833   TGTGCATCTG CGTACTGGCT TGAACAGATG GCAGAACCAC AGATAGATGT AGAAGTTTCT          5560
834
835   CCATTTTGTG TGTTCTGGGA GCTCATGGAT ATTCCAGGAC ACAAAAGGTG GAGAAGAGCT          5620
836
837   TTGTTCATCC TCTTAGCAGA TAAACGTCCT CAAAACTGGG TTGGACTTAC TAAAGTAAAA          5680
838
839   TGAAAATCTA ATATTTGTTA TATTATTTTC AAAGGTCTAT AATAACACAC TCCTTAGTAA          5740
840
841   CTTATGTAAT GTTATTTTAA AGAATTGGTG ACTAAATACA AAGTAATTAT GTCATAAACC          5800
842
843   CCTGAACATA ATGTTGTCTT ACATTTGCAG  AA TGT GAG GAA ATT ATC AGG AAA          5853
844                                      Glu Cys Glu Glu Ile Ile Arg Lys
845                                      240                 245
846
847   GGA GGT GAA ACA TCT GAA ATG TAT CTC ATT CAA CCT GAC AGT TCT GTC          5901
848   Gly Gly Glu Thr Ser Glu Met Tyr Leu Ile Gln Pro Asp Ser Ser Val
849            250                 255                 260
850
851   AAA CCG TAT AGA GTA TAC TGT GAC ATG AAT ACA GAA AAT GGA  G              5944
852   Lys Pro Tyr Arg Val Tyr Cys Asp Met Asn Thr Glu Asn Gly
853            265                 270                 275
854
855   GTAAGCTTTC GACAGTTGTT GACCTGTTGA TCTGTAATTA TTTGGATACC GTAAAATGCC          6004
856
857   AGGAAACAAG GCCAGGTGTG GTGGCTCATA CCTGTAATTC CAGCACCTTG GGAGGCCAAA          6064
858
859   GTGGGCTGAT AGCTTGAGCC TAGGAGTTTG AAACTAGCCT GGGCAACATA ATGAGACCCT          6124
860
861   AACTCTACAA AAAAAAAAA AATACCAAAA AAAAAAAAA AATCAGCTGT GTTGGTAGTA          6184
862
863   TGTGCCTGTA GTCCCAGCTA TCCAGGAGGC TGAGATGGGA GATCACCTGA GCCCACAACC          6244
864
865   TGGAGTCTTG ATCATGCTAC TGAACTGTAG CCTGGGCAAC AGAGGATAGT GAGATCCTGT          6304
866
867   CTCAAAAAAA AAAATTAATT AAAAAGCCAG GAAACAAGAC TTAGCTCTAA CATCTAACAT          6364
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868
869   AGCTGACAAA GGAGTAATTT GATGTGGAAT TCAACCTGAT ATTTAAAAGT TATAAAATAT        6424
870
871   CTATAATTCA CAATTTGGGG TAAGATAAAG CACTTGCAGT TTCCAAAGAT TTTACAAGTT        6484
872
873   TACCTCTCAT ATTTATTTCC TTATTGTGTC TATTTTAGAG CACCAAATAT ATACTAAATG        6544
874
875   GAATGGACAG GGGATTCAGA TATTATTTTC AAAGTGACAT TATTTGCTGT TGGTTAATAT        6604
876
877   ATGCTCTTTT TGTTTCTGTC AACCAAAG  GA TGG ACA GTG ATT CAG AAC CGT           6655
878                                    Gly Trp Thr Val Ile Gln Asn Arg
879                                                 280             285
880
881   CAA GAC GGT AGT GTT GAC TTT GGC AGG AAA TGG GAT CCA TAT AAA CAG         6703
882   Gln Asp Gly Ser Val Asp Phe Gly Arg Lys Trp Asp Pro Tyr Lys Gln
883               290             295             300
884
885   GGA TTT GGA AAT GTT GCA ACC AAC ACA GAT GGG AAG AAT TAC TGT GGC         6751
886   Gly Phe Gly Asn Val Ala Thr Asn Thr Asp Gly Lys Asn Tyr Cys Gly
887           305             310             315
888
889   CTA CCA  G GTAACGAACA GGCATGCAAA ATAAAATCAT TCTATTTGAA ATGGGATTTT       6808
890   Leu Pro
891
892
893   TTTTAATTAA AAAACATTCA TTGTTGGAAG CCTGTTTTAG GCAGTTAAGA GGAGTTTCCT        6868
894
895   GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT        6928
896
897   TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG  GT GAA TAT TGG CTT          6980
898                                             Gly Glu Tyr Trp Leu
899                                                    320
900
901   GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT        7028
902   Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu
903   325             330             335             340
904
905   TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT        7076
906   Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr
907               345             350             355
908
909   GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG        7124
910   Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val
911               360             365             370
912
913   AAC AAA TAC AGA GGA ACA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT        7172
914   Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met Asp Gly Ala Ser
915           375             380             385
916
917   CAG CTG ATG GGA GAA AAC AGG ACC ATG ACC ATT CAC AAC GGC ATG TTC        7220
918   Gln Leu Met Gly Glu Asn Arg Thr Met Thr Ile His Asn Gly Met Phe
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919          390                    395                    400
920
921    TTC AGC ACG TAT GAC AGA GAC AAT GAC GGC   TG  GTATGTGTGG           7262
922    Phe Ser Thr Tyr Asp Arg Asp Asn Asp Gly   Trp
923    405                 410                    415
924
925    CACTCTTTGC TCCTGCTTTA AAAATCACAC TAATATCATT ACTCAGAATC ATTAACAATA    7322
926
927    TTTTTAATAG CTACCACTTC CTGGGCACTT ACTGTCAGCC ACTGTCCTAA GCTCTTTATG    7382
928
929    CATCACTCGA AAGCATTTCA ACTATAAGGT AGACATTCTT ATTCTCATTT TACAGATGAG    7442
930
931    ATTTAGAGAG ATTACGTGAT TTGTCCAATG TCACACAACT ACCCAGAGAT AAAACTAGAA    7502
932
933    TTTGAGCACA GTTACTTTCT GAATAATGAG CATTTAGATA AATACCTATA TCTCTATATT    7562
934
935    CTAAAGTGTG TGTGAAAACT TTCATTTTCA TTTCCAGGGT TCTCTGATAC TAAGGGTTGT    7622
936
937    AAAAGCTATT ATTCCAGTAT AAAGTAACAA ACACAGTCCC TAGATGGATT GCCACAAAGG    7682
938
939    CCCAGTTATC TCTCTTTCTT GCTATAGGGC ACAGGAGGTC TTTGGTGTAT TAGTGTGACT    7742
940
941    CTATGTATAG CACCCAAAGG AAAGACTACT GTGCACACGA GTGTAGCAGT CTTTTATGGG    7802
942
943    TAATCTGCAA AACGTAACTT GACCACCGTA GTTCTGTTTC TAATAACGCC AAACACATTT    7862
944
945    TCTTTCAG G TTA ACA TCA GAT CCC AGA AAA CAG TGT TCT AAA GAA GAC       7910
946             Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp
947                          420                    425
948
949    GGT GGT GGA TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC     7958
950    Gly Gly Gly Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly
951      430                 435                    440
952
953    AGA TAC TAC TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC     8006
954    Arg Tyr Tyr Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly
955    445                 450                    455                 460
956
957    ACA GAT GAT GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA     8054
958    Thr Asp Asp Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser
959                      465                    470                 475
960
961    ATG AGG AAG ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTCCCCAA   8109
962    Met Arg Lys Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln
963                      480                    485                 490
964
965    TACGTAGATT TTTGCTCTTC TGTATGTGAC AACATTTTTG TACATTATGT TATTGGAATT    8169
966
967    TTCTTTCATA CATTATATTC CTCTAAAACT CTCAAGCAGA CGTGAGTGTG ACTTTTTGAA    8229
968
969    AAAAGTATAG GATAAATTAC ATTAAAATAG CACATGATTT TCTTTTGTTT TCTTCATTTC    8289
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970
971  TCTTGCTCAC CCAAGAAGTA ACAAAAGTAT AGTTTTGACA GAGTTGGTGT TCATAATTTC   8349
972
973  AGTTCTAGTT GATTGCGAGA ATTTTCAAAT AAGGAAGAGG GGTCTTTTAT CCTTGTCGTA   8409
974
975  GGAAAACCAT GACGGAAAGG AAAAACTGAT GTTTAAAAGT CCACTTTTAA AACTATATTT   8469
976
977  ATTTATGTAG GATCTGTCAA AGAAAACTTC CAAAAAGATT TATTAATTAA ACCAGACTCT   8529
978
979  GTTGCAATAA GTTAATGTTT TCTTGTTTTG TAATCCACAC ATTCAATGAG TTAGGCTTTG   8589
980
981  CACTTGTAAG GAAGGAGAAG CGTTCACAAC CTCAAATAGC TAATAAACCG GTCTTGAATA   8649
982
983  TTTGAAGATT TAAAATCTGA CTCTAGGACG GGCACGGTGG CTCACGACTA TAATCCCAAC   8709
984
985  ACTTTGGGAG GCTGAGGCGG GCGGTCACAA GGTCAGGAGT TCAAGACCAG CCTGACCAAT   8769
986
987  ATGGTGAAAC CCCATCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGCAGGTGCC   8829
988
989  TGTAGGTCCC AGCTAGCCTG TGAGGTGGAG ATTGCATTGA GCCAAGATC              8878
990
991
992  (2) INFORMATION FOR SEQ ID NO:4:
993
994        (i) SEQUENCE CHARACTERISTICS:
995            (A) LENGTH: 491 amino acids
996            (B) TYPE: amino acid
997            (D) TOPOLOGY: linear
998
999        (ii) MOLECULE TYPE: protein
1000
1001       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
1002
1003  Met Lys Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys
1004   1               5                   10                  15
1005
1006  His Leu Leu Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly
1007               20                  25                  30
1008
1009  Val Asn Asp Asn Glu Glu Gly Phe Phe Ser Ala Arg Gly His Arg Pro
1010           35                  40                  45
1011
1012  Leu Asp Lys Lys Arg Glu Glu Ala Pro Ser Leu Arg Pro Ala Pro Pro
1013       50                  55                  60
1014
1015  Pro Ile Ser Gly Gly Gly Tyr Arg Ala Arg Pro Ala Lys Ala Ala Ala
1016   65                  70                  75                  80
1017
1018  Thr Gln Lys Lys Val Glu Arg Lys Ala Pro Asp Ala Gly Gly Cys Leu
1019               85                  90                  95
1020
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/206,176*

INPUT SET: S1765.raw

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1021   His Ala Asp Pro Asp Leu Gly Val Leu Cys Pro Thr Gly Cys Gln Leu
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1023
1024   Gln Glu Ala Leu Leu Gln Gln Glu Arg Pro Ile Arg Asn Ser Val Asp
1025           115             120             125
1026
1027   Glu Leu Asn Asn Asn Val Glu Ala Val Ser Gln Thr Ser Ser Ser Ser
1028       130             135             140
1029
1030   Phe Gln Tyr Met Tyr Leu Leu Lys Asp Leu Trp Gln Lys Arg Gln Lys
1031   145             150             155             160
1032
1033
1034   Gln Val Lys Asp Asn Glu Asn Val Val Asn Glu Tyr Ser Ser Glu Leu
1035           165             170             175
1036
1037   Glu Lys His Gln Leu Tyr Ile Asp Glu Thr Val Asn Ser Asn Ile Pro
1038           180             185             190
1039
1040   Thr Asn Leu Arg Val Leu Arg Ser Ile Leu Glu Asn Leu Arg Ser Lys
1041           195             200             205
1042
1043   Ile Gln Lys Leu Glu Ser Asp Val Ser Ala Gln Met Glu Tyr Cys Arg
1044       210             215             220
1045
1046   Thr Pro Cys Thr Val Ser Cys Asn Ile Pro Val Val Ser Gly Lys Glu
1047   225             230             235             240
1048
1049   Cys Glu Glu Ile Ile Arg Lys Gly Gly Glu Thr Ser Glu Met Tyr Leu
1050               245             250             255
1051
1052   Ile Gln Pro Asp Ser Ser Val Lys Pro Tyr Arg Val Tyr Cys Asp Met
1053           260             265             270
1054
1055   Asn Thr Glu Asn Gly Gly Trp Thr Val Ile Gln Asn Arg Gln Asp Gly
1056       275             280             285
1057
1058   Ser Val Asp Phe Gly Arg Lys Trp Asp Pro Tyr Lys Gln Gly Phe Gly
1059       290             295             300
1060
1061   Asn Val Ala Thr Asn Thr Asp Gly Lys Asn Tyr Cys Gly Leu Pro Gly
1062   305             310             315             320
1063
1064   Glu Tyr Trp Leu Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly
1065           325             330             335
1066
1067   Pro Thr Glu Leu Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val
1068           340             345             350
1069
1070   Lys Ala His Tyr Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr
1071           355             360             365
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1072
1073    Gln Ile Ser Val Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met
1074        370             375             380
1075
1076    Asp Gly Ala Ser Gln Leu Met Gly Glu Asn Arg Thr Met Thr Ile His
1077    385             390             395             400
1078
1079    Asn Gly Met Phe Phe Ser Thr Tyr Asp Arg Asp Asn Asp Gly Trp Leu
1080                405             410             415
1081
1082    Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp Gly Gly Gly Trp
1083                420             425             430
1084
1085    Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly Arg Tyr Tyr Trp
1086        435             440             445
1087
1088    Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly Thr Asp Asp Gly
1089        450             455             460
1090
1091    Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser Met Arg Lys Met
1092    465             470             475             480
1093
1094    Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln
1095                485             490
1096
1097
1098    (2) INFORMATION FOR SEQ ID NO:5:
1099
1100        (i) SEQUENCE CHARACTERISTICS:
1101            (A) LENGTH: 10564 base pairs
1102            (B) TYPE: nucleic acid
1103            (C) STRANDEDNESS: double
1104            (D) TOPOLOGY: linear
1105
1106        (ii) MOLECULE TYPE: DNA (genomic)
1107
1108
1109        (vii) IMMEDIATE SOURCE:
1110            (B) CLONE: human fibrinogen gamma chain
1111
1112        (ix) FEATURE:
1113            (A) NAME/KEY: CDS
1114            (B) LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
1115                ..2603, 4211..4341, 4645..4778, 5758..5942, 7426
1116                ..7703, 9342..9571)
1117
1118
1119        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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1121    CTACACACTT CTTGAAGGCA AAGGCAATGC TGAAGTCACC TTTCATGTTC AAATCATATT        60
1122
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INPUT SET: S1765.raw

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1123  AAAAAGTTAG CAAGATGTAA TTATCAGTGT ACTATGTAAA TCTTTGTGAA TGATCAATAA    120
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1125  TTACATATTT TCATTATATA TATTTTAGTA GATAATATTT ATATACATTC AACATTCTAA    180
1126
1127  ATATAGAAAG TTTACAGAGA AAAATAAAGC CTTTTTTTCC AATCCTGTCC TCCACCTCTG    240
1128
1129  CATCCCATTC TTCTTCACAG AGGCAACTGA TTCAAGTCAT TACATAGTTA TTGAGTGTTA    300
1130
1131  ACTACAACTA TGTTAAGTAC AGCTATATAT GTTAGATGCC GTAGCCACAG AAATCAGTTT    360
1132
1133  ACAATCTAAT GCAGTGGATA CAGCATGTAT ACATATAATA TAAGGTTGCT ACAAATGCTA    420
1134
1135  TCTGAGGTAG AGCTGTTTGA AAGAATACTA ATACTTAAAT GTTTAATTCA ACTGACTTGA    480
1136
1137  TTGACAACTG ATTAGCTGAG TGGAAAAGAT GGATGAGAAA GATTGTGAGA CTTAATTGGC    540
1138
1139  TGGTGGTATG GTGATATGAT TGACAATAAC TGCTAAGTCA GAGAGGGATA TATTAAGGAG    600
1140
1141  GAGAAGAAAA GCAACAAATC TGGTTTTGAT GTGTTCACTT TGTTATAATT ATTGATTATT    660
1142
1143  TACTGAATAT GAATATTTAT CTTTGTTTTT GAGTCAATAA ATATACCTTT GTAAAGACAG    720
1144
1145  AATTAAAGTA TTAGTATTTC TTTCAAACTG GAGGCATTTC TCCCACTAAC ATATTTCATC    780
1146
1147  AAAACTTATA ATAAGCTTGG TTCCAGAGGA AGAAATGAGG GATAACCAAA AATAGAGACA    840
1148
1149  TTAATAATAG TGTAACGCCC AGTGATAAAT CTCAATAGGC AGTGATGACA GACATGTTTT    900
1150
1151  CCCAAACACA AGGATGCTGT AAGGGCCAAA CAGAAATGAT GGCCCCTCCC CAGCACCTCA    960
1152
1153  TTTTGCCCCT TCCTTCAGCT ATGCCTCTAC TCTCCTTTAG ATACAAGGGA GGTGGATTTT    1020
1154
1155  TCTCTTCTCT GAGATAGCTT GATGGAACCA CAGGAACAAT GAAGTGGGCT CCTGGCTCTT    1080
1156
1157  TTCTCTGTGG CAGATGGGGT GCCATGCCCA CCTTCAGACA AAGGGAAGAT TGAGCTCAAA    1140
1158
1159  AGCTCCCTGA GAAGTGAGAG CCTATGAACA TGGTTGACAC AGAGGGACAG GAATGTATTT    1200
1160
1161  CCAGGGTCAT TCATTCCTGG GAATAGTGAA CTGGGACATG GGGGAAGTCA GTCTCCTCCT    1260
1162
1163  GCCACAGCCA CAGATTAAAA ATAATAATGT TAACTGATCC CTAGGCTAAA ATAATAGTGT    1320
1164
1165  TAACTGATCC CTAAGCTAAG AAAGTTCTTT TGGTAATTCA GGTGATGGCA GCAGGACCCA    1380
1166
1167  TCTTAAGGAT AGACTAGGTT TGCTTAGTTC GAGGTCATAT CTGTTTGCTC TCAGCCATGT    1440
1168
1169  ACTGGAAGAA GTTGCATCAC ACAGCCTCCA GGACTGCCCT CCTCCTCACA GCAATGGATA    1500
1170
1171  ATGCTTCACT AGCCTTTGCA GATAATTTTG GATCAGAGAA AAAACCTTGA GCTGGGCCAA    1560
1172
1173  AAAGGAGGAG CTTCAACCTG TGTGCAAAAT CTGGGAACCT GACAGTATAG GTTGGGGGCC    1620
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/206,176

INPUT SET: S1765.raw

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1175   AGGATGAGGA AAAAGGAACG GGAAAGACCT GCCCACCCTT CTGGTAAGGA GGCCCCGTGA      1680
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1177   TCAGCTCCAG CCATTTGCAG TCCTGGCTAT CCCAGGAGCT TACATAAAGG GACAATTGGA      1740
1178
1179   GCCTGAGAGG TGACAGTGCT GACACTACAA GGCTCGGAGC TCCGGGCACT CAGACATC        1798
1180
1181   ATG AGT TGG TCC TTG CAC CCC CGG AAT TTA ATT CTC TAC TTC TAT GCT        1846
1182   Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala
1183    1           5               10              15
1184
1185   CTT TTA TTT CTC TCT TCA ACA TGT GTA GCA GTAAGTGTGC TCTTCACAAA          1896
1186   Leu Leu Phe Leu Ser Ser Thr Cys Val Ala
1187            20              25
1188
1189   ACGTTGTTTA AAATGGAAAG CTGGAAAATA AAACAGATAA TAAACTAGTG AAATTTTCGT       1956
1190
1191   ATTTTTTCTC TTTTAG TAT GTT GCT ACC AGA GAC AAC TGC TGC ATC TTA          2005
1192                 Tyr Val Ala Thr Arg Asp Asn Cys Cys Ile Leu
1193                         30              35
1194
1195   GAT GAA AGA TTC GTAAGTAGTT TTTATGTTTC TCCCTTTGTG TGTGAACTGG            2057
1196   Asp Glu Arg Phe
1197            40
1198
1199   AGAGGGGCAG AGGAATAGAA ATAATTCCCT CATAAATATC ATCTGGCACT TGTAACTTTT       2117
1200
1201   TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC       2177
1202
1203   TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT        2230
1204                                 Gly Ser Tyr Cys Pro Thr Thr Cys
1205                                             45
1206
1207   GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT        2278
1208   Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp
1209    50              55              60                      65
1210
1211   CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA        2326
1212   Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser
1213                70              75              80
1214
1215   GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT        2374
1216   Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp
1217                85              90              95
1218
1219   GAA TCA TCA AAA CCA  A GTGAGAAAT AAAGACTACT GACCAAAAAA                 2420
1220   Glu Ser Ser Lys Pro
1221            100
1222
1223   TAATAATAAT AATCTGTGAA GTTCTTTTGC TGTTGTTTTA GTTGTTCTAT TTGCTTAAGG      2480
1224
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/206,176*

INPUT SET: S1765.raw

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1225   ATTTTTATGT CTCTGATCCT ATATTACAG  AT ATG ATA GAC GCT GCT ACT TTG    2532
1226                                        Asn Met Ile Asp Ala Ala Thr Leu
1227                                            105                     110
1228
1229   AAG TCC AGG ATA ATG TTA GAA GAA ATT ATG AAA TAT GAA GCA TCG ATT     2580
1230   Lys Ser Arg Ile Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile
1231                   115                 120                 125
1232
1233   TTA ACA CAT GAC TCA AGT ATT  CG GTAAGGATTT TTGTTTTAAT TTGCTCTGCA    2633
1234   Leu Thr His Asp Ser Ser Ile Arg
1235                   130
1236
1237   AGACTGATTT AGTTTTTATT TAATATTCTA TACTTGAGTG AAAGTAATTT TTAATGTGTT    2693
1238
1239   TTCCCCATTT ATAATATCCC AGTGACATTA TGCCTGATTA TGTTGAGCAT AGTAGAGATA    2753
1240
1241   GAAGTTTTTA GTGCAATATA AATTATACTG GGTTATAATT GCTTATTAAT AATCACATTG    2813
1242
1243   AAGAAAGATG TTCTAGATGT CTTCAAATGC TAGTTTGACC ATATTTATCA AAAATTTTTT    2873
1244
1245   CCCCATCCCC CATTTATCTT ACAACATAAA ATCAATCTCA TAGGAATTTG GGTGTTGAAA    2933
1246
1247   ATAAAATCCT CTTTATAAAA ATGCTGACAA ATTGGTGGTT AAAAAAATTA GCAAGCAGAG    2993
1248
1249   GCATAGTAAG GATTTTGGCT CCTAAAGTAA ATTATATTGA ATGTGGAGCA GGAAGAAACA    3053
1250
1251   TGTCTTGAGA GACTAAGTGT GGCAAATATT GCAAAGCTCA TATTGATCAT TGCAGAATGA    3113
1252
1253   ACCTGCATAG TCTCTTCCCT TCATTTGGAA GTGAATGTCT CTGTTAAAGC TTCTCAGGGA    3173
1254
1255   CTCATAAACT TTCTGAACAT AAGGTCTCAG ATACAGTTTT AATATTTTTC CCCAATTTTT    3233
1256
1257   TTTTCTGAAT TTTTCTCAAA GCAGCTTGAG AAATTGAGAT AAATAGTAGC TAGGGAGAAG    3293
1258
1259   TGGCCCAGGA AAGATTTCTC CTCTTTTTGC TATCAGAGGG CCCTTGTTAT TATTGTTATT    3353
1260
1261   ATTATTACTT GCATTATTAT TGTCCATCAT TGAAGTTGAA GGAGGTTATT GTACAGAAAT    3413
1262
1263   TGCCTAAGAC AAGGTAGAGG GAAAACGTGG ACAAATAGTT TGTCTACCCT TTTTTACTTC    3473
1264
1265   AAAGAAAGAA CGGTTTATGC ATTGTAGACA GTTTTCTATC ATTTTTGGAT ATTTGCAAGC    3533
1266
1267   CACCCTGTAA GTAACTACAA AAGGAGGGTT TTTACTTCCC CCAGTCCATT CCCAAAGCTA    3593
1268
1269   TGTAACCAGA AGCATTAAAG AAGAAAGGGG AAGTATCTGT TGTTTTATTT TACATACAAT    3653
1270
1271   AACGTTCCAG ATCATGTCCC TGTGTAAGTT ATATTTTAGA TTGAAGCTTA TATGTATAGC    3713
1272
1273   CTCAGTAGAT CCACAAGTGA AAGGTATACT CCTTCAGCAC ATGTGAATTA CTGAACTGAG    3773
1274
1275   CTTTTCCTGC TTCTAAAGCA TCAGGGGGTG TTCCTATTAA CCAGTCTCGC CACTCTTGCA    3833
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1276
1277   GGTTGCTATC TGCTGTCCCT TATGCATAAA GTAAAAAGCA AAATGTCAAT GACATTTGCT   3893
1278
1279   TATTGACAAG GACTTTGTTA TTTGTGTTGG GAGTTGAGAC AATATGCCCC ATTCTAAGTA   3953
1280
1281   AAAAGATTCA GGTCCACATT GTATTCCTGT TTTAATTGAT TTTTTGATTT GTTTTTCTTT   4013
1282
1283   TTCAAAAAGT TTATAATTTT AATTCATGTT AATTTAGTAA TATAATTTTA CATTTTCCTC   4073
1284
1285   AAGAATGGAA TAATTTATCA GAAAGCACTT CTTAAGAAAA TACTTAGCAG TTTCCAAAGA   4133
1286
1287   AAATATAAAA TTACTCTTCT GAAAGGAATA CTTATTTTTG TCTTCTTATT TTTGTTATCT   4193
1288
1289   TATGTTTCTG TTTGTAG A TAT TTG CAG GAA ATA TAT AAT TCA AAT AAT CAA       4244
1290                      Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn Gln
1291                      135             140                 145
1292
1293   AAG ATT GTT AAC CTG AAA GAG AAG GTA GCC CAG CTT GAA GCA CAG TGC      4292
1294   Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln Cys
1295            150             155             160
1296
1297   CAG GAA CCT TGC AAA GAC ACG GTG CAA ATC CAT GAT ATC ACT GGG AAA  G  4341
1298   Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly Lys
1299            165             170             175
1300
1301   GTAACTGATG AAGGTTATAT TGGGATTAGG TTCATCAAAG TAAGTAATGT AAAGGAGAAA   4401
1302
1303   GTATGTACTG GAAAGTATAG GAATAGTTTA GAAAGTGGCT ACCCATTAAG TCTAAGAATT   4461
1304
1305   TCAGTTGTCT AGACCTTTCT TGAATAGCTA AAAAAAACAG TTTAAAAGGA ATGCTGATGT   4521
1306
1307   GAAAAGTAAG AAAATTATTC TTGGAAAATG AATAGTTTAC TACATGTTAA AAGCTATTTT   4581
1308
1309   TCAAGGCTGG CACAGTCTTA CCTGCATTTC AAACCACAGT AAAAGTCGAT TCTCCTTCTC   4641
1310
1311   TAG  AT TGT CAA GAC ATT GCC AAT AAG GGA GCT AAA CAG AGC GGG CTT     4688
1312        Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu
1313            180             185             190
1314
1315   TAC TTT ATT AAA CCT CTG AAA GCT AAC CAG CAA TTC TTA GTC TAC TGT     4736
1316   Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys
1317            195             200             205
1318
1319   GAA ATC GAT GGG TCT GGA AAT GGA TGG ACT GTG TTT CAG AAG             4778
1320   Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys
1321            210             215             220
1322
1323   GTAATTTTTT CCCCACCATG TGTATTTAAT AAATTCCTAC ATTGTTTCTG CCATATGGCA   4838
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1325   GATACTTTTC TAAGCACCTT GTGAACCGTA GCTCATTTAA TCCTTGCAAT AGCCCTAAGA   4898
1326
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INPUT SET: S1765.raw

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1327  GGAAGGTACT TCTGTTACTC CTATTTACAG AAAAGGAAAC TGAGGCACAC AAGGTTAAAT    4958
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1329  AACTTGCCCA AGACCACATA ACTAATAAGC AACAGAGTCA GCATTTGAAC CTAGGCAGTA    5018
1330
1331  TAGTTTCAGA GTTTGTGACT TGACTCTATA TTGTACTGGC ACTGACTTTG TAGATTCATG    5078
1332
1333  GTGGCACATA ATCATAGTAC CACAGTGACA AATAAAAAGA AGGAAACTCT TTTGTCAGGT    5138
1334
1335  AGGTCAAGAC CTGAGGTTTC CCATCACAAG ATGAGGAAGC CCAACACCAC CCCCCACCAC    5198
1336
1337  CCCACCACCA TCACCACCCT TTCACACACC AGAGGATACA CTTGGGCTGC TCCAAGACAA    5258
1338
1339  GGAACCTGTG TTGCATCTGC CACTTGCTGA TACCCACTAG GAATCTTGGC TCCTTTACTT    5318
1340
1341  TCTGTTTACC TCCCACCACT GTTATAACTG TTTCTACAGG GGGCGCTCAG AGGGAATGAA    5378
1342
1343  TGGTGGAAGC ATTAGTTGCC AGACACCGAT TGAGCAATGG GTTCCATCAT AAGTGTAAGA    5438
1344
1345  ATCAGTAATA TCCAGCTAGA GTTCTGAAGT CGTCTAGGTG TCTTTTTAAT ATTACCACTC    5498
1346
1347  ATTTAGAATT TATGATGTGC CAGAAACCCT CTTAAGTATT TCTCTTATAT TCTCTCTCAT    5558
1348
1349  GATCCTTGCA GCAACCCTAA GAAGTAACCA TCATTTTTCC TATTTGATAC ATGAGGAAAC    5618
1350
1351  TGAGGTAGCT TGGCCAAGAT CACTTAGTTG GGAGTTGATA GAACCAGTGC TCTGTATTTT    5678
1352
1353  TGACAAAATG TTGACAGCAT TCTCTTTACA TGCATTGATA GTCTATTTTC TCCTTTTGCT    5738
1354
1355  CTTGCAAATG TGTAATTAG AGA CTT GAT GGC AGT GTA GAT TTC AAG AAA AAC     5790
1356                        Arg Leu Asp Gly Ser Val Asp Phe Lys Lys Asn
1357                                     225                 230
1358
1359  TGG ATT CAA TAT AAA GAA GGA TTT GGA CAT CTG TCT CCT ACT GGC ACA     5838
1360  Trp Ile Gln Tyr Lys Glu Gly Phe Gly His Leu Ser Pro Thr Gly Thr
1361      235                 240                 245
1362
1363  ACA GAA TTT TGG CTG GGA AAT GAG AAG ATT CAT TTG ATA AGC ACA CAG     5886
1364  Thr Glu Phe Trp Leu Gly Asn Glu Lys Ile His Leu Ile Ser Thr Gln
1365  250                 255                 260                 265
1366
1367  TCT GCC ATC CCA TAT GCA TTA AGA GTG GAA CTG GAA GAC TGG AAT GGC     5934
1368  Ser Ala Ile Pro Tyr Ala Leu Arg Val Glu Leu Glu Asp Trp Asn Gly
1369                  270                 275                 280
1370
1371  AGA ACC  AG  GTACTGTTTT GAAATGACTT CCAACTTTTT ATTGTAAAGA            5982
1372  Arg Thr  Ser
1373
1374
1375  TTGCCTGGAA TGTGCACTTT CCAACTATCA ATAGACAATG GCAAATGCAG CCTGACAAAT    6042
1376
1377  GCAAACAGCA CATCCAGCCA CCATTTTCTC CAGGAGTCTG TTTGGTTCTT GGGCAATCCA    6102
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PATENT APPLICATION   US/08/206,176

INPUT SET: S1765.raw

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1380
1381   ACCATTCAGA GTAATAGCTA ATTACTGAAC TTTTAATCAG TCCCAGGAAT TGAGCATAAA      6222
1382
1383   ATTATAATTT TATCTAGTCT AAATTACTAT TTCATGAAGC AGGTATTATT ATTAATCCCA      6282
1384
1385   TTTTATAGAT TAACTTGCTC AAAGTCACAT TGCTGATAAG TGGTAGAGGT AGAATTCAGA      6342
1386
1387   CTCAAGTAGT TTAACTTTAG AGCCTGTCCT CTTAACAACT ATCCTGGTTG AAAAGCAAAT      6402
1388
1389   ACAGCCTCTT CAGACTTCTC AGTGCCTTGA TGGCCATTTA TTCTGTCAAA TCATGAGCTA      6462
1390
1391   CCCTAAAAGT AAACCAGCTA GCTCTTTTGA TGATCTAGAG GCTTCTTTTT GCTTGAGATA      6522
1392
1393   TTTGAAGGTT TTAAGCATTG TTACCTAATT AAAATGCAGA AAAATATCCA ACCCTCTTGT      6582
1394
1395   TATGTTTAAG GAATAGTGAA ATATATTGTC TTCAAACACA TGGACTTTTT TTTATTGCTT      6642
1396
1397   GGTTGGTTTT TAATCCAGAA AGTGCTATAG TCAGTAGACC TTCTTCTAGG AAAGGACCTT      6702
1398
1399   CCATTTCCCA GCCACTGGAG ATTAGAAAAT AAGCTAAATA TTTTCTGGAA ATTTCTGTTC      6762
1400
1401   ATTCATTAAG GCCCATCCTT TCCCCCACTC TATAGAAGTG TTGTCCACTT GCACAATTTT      6822
1402
1403   TTCCAGGAAA GAATCTCTCT AACTCCTTCA GCTCACATGC TTTGGACCAC ACAGGGAAGA      6882
1404
1405   CTTTGATTGT GTAATGCCCT CAGAAGCTCT CCTTCTTGCC ACTACCACAC TGATTTGAGG      6942
1406
1407   AAGAAAATCC CTTTAGCACC TAACCCTTCA GGTGCTATGA GTGGCTAATG GAACTGTACC      7002
1408
1409   TCCTTCAAGT TTTGTGCAAT AATTAAGGGT CACTCACTGT CAGATACTTT CTGTGATCTA      7062
1410
1411   TGATAATGTG TGTGCAACAC ATAACATTTC AATAAAAGTA GAAAATATGA AATTAGAGTC      7122
1412
1413   ATCTACACAT CTGGATTTGA TCTTAGAATG AAACAAGCAA AAAAGCATCC AAGTGAGTGC      7182
1414
1415   AATTATTAGT TTTCAGAGAT GCTTCAAAGG CTTCTAGGCC CATCCCGGGA AGTGTTAATG      7242
1416
1417   AGCTGTGGAC TGGTTCACAT ATCTATTGCC TCTTGCCAGA TTTGCAAAAA ACTTCACTCA      7302
1418
1419   ATGAGCAAAT TTCAGCCTTA AGAAACAAAG TCAAAAATTC CAAGGAAGCA TCCTACGAAA      7362
1420
1421   GAGGGAACTT CTGAGATCCC TGAGGAGGGT CAGCATGTGA TGGTTGTATT TCCTTCTTCT      7422
1422
1423   CAG T ACT GCA GAC TAT GCC ATG TTC AAG GTG GGA CCT GAA GCT GAC          7468
1424         Thr Ala Asp Tyr Ala Met Phe Lys Val Gly Pro Glu Ala Asp
1425          285                 290                 295
1426
1427   AAG TAC CGC CTA ACA TAT GCC TAC TTC GCT GGT GGG GAT GCT GGA GAT      7516
1428   Lys Tyr Arg Leu Thr Tyr Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp
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PATENT APPLICATION   US/08/206,176

INPUT SET: S1765.raw

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1429        300                    305                    310
1430
1431   GCC TTT GAT GGC TTT GAT TTT GGC GAT GAT CCT AGT GAC AAG TTT TTC      7564
1432   Ala Phe Asp Gly Phe Asp Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe
1433   315                    320                    325                    330
1434
1435   ACA TCC CAT AAT GGC ATG CAG TTC AGT ACC TGG GAC AAT GAC AAT GAT      7612
1436   Thr Ser His Asn Gly Met Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp
1437                      335                    340                    345
1438
1439   AAG TTT GAA GGC AAC TGT GCT GAA CAG GAT GGA TCT GGT TGG TGG ATG      7660
1440   Lys Phe Glu Gly Asn Cys Ala Glu Gln Asp Gly Ser Gly Trp Trp Met
1441                      350                    355                    360
1442
1443   AAC AAG TGT CAC GCT GGC CAT CTC AAT GGA GTT TAT TAC CAA  G           7703
1444   Asn Lys Cys His Ala Gly His Leu Asn Gly Val Tyr Tyr Gln
1445                365                    370                    375
1446
1447   GTATGTTTTC CTTTCTTAGA TTCCAAGTTA ATGTATAGTG TATACTATTT TCATAAAAAA    7763
1448
1449   TAATAAATAG ATATGAAGAA ATGAAGAATA ATTTATAAAG ATAGTAGGGA TTTTATCATG    7823
1450
1451   TTCTTTATTT CAACTAAGTT CTTTGAAACT GGAAGTGGAT AATACCAAGT TCATGCCTAA    7883
1452
1453   AATTAGCCCT TCTAAAGAAA TCCACCTGCT GCAAAATATC CAGTAGTTTG GCATTATATG    7943
1454
1455   TGAAACTATC ACCATCATAG CTGGCACTGT GGGTTGTGGG ATCTCCTTTA GACATACAAC    8003
1456
1457   ATAAATGATC TGGATGGATT AACATTACTA CATGGATGCT TGTTGACACA TTAACCTGGC    8063
1458
1459   TTCCCATGAG CTTTGTGTCA GATACACGCA GTGAACAGGT GTTTGGAGGA ACAGAATAAA    8123
1460
1461   GAGAAGGCAA GCACTGGTAA GGGCAGGGGT TTGTGAAAGC TTGAGAGAAG AGACCAGTCT    8183
1462
1463   GAGGACAGTA GACACTTATT TTAGGATGGG GGTTGGATGA GGAGGCTATA GTTTGCTATA    8243
1464
1465   AGCTTGGAAT GGTTTGGAAC ACTGGTTTCA CTCACCTACC CAGCAGTTAT GTGTGGGGAA    8303
1466
1467   GCCTTACCGA TGCTAAAGGA TCCATGTTAC AATAATGGCA TTATTTGGAA ATCCCAGTGG    8363
1468
1469   TATTCCATGA ATAAAACCAC TATGAAGATA ATCCCACTCA ACAGACTCTC CGTTGGAGAA    8423
1470
1471   GGACAGCAAC ACCACCCTGG GAAAGCCAAA CAGTCAGACC AGACCTGTTT AGCATCAGTA    8483
1472
1473   GGACTTCCCT ACCATATCTG CTGGGTAGAT GAGTGAAACC AGTGTTCCAA ACCACTCCGG    8543
1474
1475   GCTTGTAGCA AACCATAGTC TCCTCATCTA CCAAGATGAG CAACCTTACC TCCTGATGTC    8603
1476
1477   CTAGCCAATC ACCAACTAGG AAACTTTGCA CAGTTTATTT AAAGTAACAG TTTGATTTTC    8663
1478
1479   ACAATATTTT TAAATTGGAG AAACATAACT TATCTTTGCA CTCACAAACC ACATAATGAG    8723
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INPUT SET: S1765.raw

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1483    GTTCATGCCA GTGTTGTGCT CTGACAAGCC TTTTACAGAA TTACATGAGA TCTGCTTCCC    8843
1484
1485    TAGGACAAGG AGAAGGCAAA TCAACAGAGG CTGCACTTTA AAATGGAGAC ATAAAATAAC    8903
1486
1487    ATGCCAGAAC CATTTCCTAA AGCTCCTCAA TCAACCAACA AAATTGTGCT TTCAAATAAC    8963
1488
1489    CTGAGTTGAC CTCATCAGGA ATTTTGTGGC TCCTTCTCTT CTAACCTGCC TGAAGAAAGA    9023
1490
1491    TGGTCCACAG CAGCTGAGTC CGGGATGGAT AAGCTTAGGG ACAGAGGCCA ATTAGGGAAC    9083
1492
1493    TTTGGGTTTC TAGCCCTACT AGTAGTGAAT AAATTTAAAG TGTGGATGTG ACTATGAGTC    9143
1494
1495    ACAGCACAGA TGTTGTTTAA TAATATGTTT ATTTTATAAA TTGATATTTT AGGAATCTTT    9203
1496
1497    GGAGATATTT TCAGTTAGCA GATAATACTA TAAATTTTAT GTAACTGGCA ATGCACTTCG    9263
1498
1499    TAATAGACAG CTCTTCATAG ACTTGCAGAG GTAAAAGAT  TCCAGAATAA TGATATGTAC    9323
1500
1501    ATCTACGACT TGTTTTAG  GT GGC ACT TAC TCA AAA GCA TCT ACT CCT AAT       9373
1502                          Gly Gly Thr Tyr Ser Lys Ala Ser Thr Pro Asn
1503                              380                 385
1504
1505    GGT TAT GAT AAT GGC ATT ATT TGG GCC ACT TGG AAA ACC CGG TGG TAT      9421
1506    Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr Arg Trp Tyr
1507        390             395                 400
1508
1509    TCC ATG AAG AAA ACC ACT ATG AAG ATA ATC CCA TTC AAC AGA CTC ACA      9469
1510    Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn Arg Leu Thr
1511        405                 410                 415
1512
1513    ATT GGA GAA GGA CAG CAA CAC CAC CTG GGG GGA GCC AAA CAG GTC AGA      9517
1514    Ile Gly Glu Gly Gln Gln His His Leu Gly Gly Ala Lys Gln Val Arg
1515    420                 425                 430                 435
1516
1517    CCA GAG CAC CCT GCG GAA ACA GAA TAT GAC TCA CTT TAC CCT GAG GAT      9565
1518    Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr Pro Glu Asp
1519                    440                 445                 450
1520
1521    GAT TTG TAGAAAATTA ACTGCTAACT TCTATTGACC CACAAAGTTT CAGAAATTCT       9621
1522    Asp Leu
1523
1524
1525    CTGAAAGTTT CTTCCTTTTT TCTCTTACTA TATTTATTGA TTTCAAGTCT TCTATTAAGG    9681
1526
1527    ACATTTAGCC TTCAATGGAA ATTAAAACTC ATTTAGGACT GTATTTCCAA ATTACTGATA    9741
1528
1529    TCAGAGTTAT TTAAAAATTG TTTATTTGAG GAGATAACAT TTCAACTTTG TTCCTAAATA    9801
1530
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1531	TATAATAATA AAATGATTGA CTTTATTTGC ATTTTTATGA CCACTTGTCA TTTATTTTGT	9861
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1533	CTTCGTAAAT TATTTTCATT ATATCAAATA TTTTAGTATG TACTTAATAA AATAGGAGAA	9921
1534		
1535	CATTTTAGAG TTTCAAATTC CCAGGTATTT TCCTTGTTTA TTACCCCTAA ATCATTCCTA	9981
1536		
1537	TTTAATTCTT CTTTTTAAAT GGAGAAAATT ATGTCTTTTT AATATGGTTT TTGTTTTGTT	10041
1538		
1539	ATATATTCAC AGGCTGGAGA CGTTTAAAAG ACCGTTTCAA AAGAGATTTA CTTTTTTAAA	10101
1540		
1541	GGACTTTATC TGAACAGAGA GATATAATAT TTTTCCTATT GGACAATGGA CTTGCAAAGC	10161
1542		
1543	TTCACTTCAT TTTAAGAGCA AAAGACCCCA TGTTGAAAAC TCCATAACAG TTTTATGCTG	10221
1544		
1545	ATGATAATTT ATCTACATGC ATTTCAATAA ACCTTTTGTT TCCTAAGACT AGATACATGG	10281
1546		
1547	TACCTTTATT GACCATTAAA AAACCACCAC TTTTTGCCAA TTTACCAATT ACAATTGGGC	10341
1548		
1549	AACCATCAGT AGTAATTGAG TCCTCATTTT ATGCTAAATG TTATGCCTAA CTCTTTGGGA	10401
1550		
1551	GTTACAAAGG AAATAGCAAT TATGGCTTTT GCCCTCTAGG AGATACAGGA CAAATACAGG	10461
1552		
1553	AAAATACAGC AACCCAAACT GACAATACTC TATACAAGAA CATAATCACT AAGCAGGAGT	10521
1554		
1555	CACAGCCACA CAACCAAGAT GCATAGTATC CAAAGTGCAG CTG	10564
1556		
1557		

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1558   (2) INFORMATION FOR SEQ ID NO:6:
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1560          (i) SEQUENCE CHARACTERISTICS:
1561              (A) LENGTH: 453 amino acids
1562              (B) TYPE: amino acid
1563              (D) TOPOLOGY: linear
1564
1565          (ii) MOLECULE TYPE: protein
1566
1567          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
1568
1569   Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala
1570    1               5                  10                  15
1571
1572   Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp
1573               20                  25                  30
1574
1575   Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr
1576           35                  40                  45
1577
1578   Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys
1579       50                  55                  60
1580
1581   Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr
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INPUT SET: S1765.raw

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1585                   85                      90                      95
1586
1587   Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser
1588                   100                     105                     110
1589
1590   Arg Ile Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr
1591               115                     120                     125
1592
1593   His Asp Ser Ser Ile Arg Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn
1594           130                     135                     140
1595
1596   Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln
1597   145                     150                     155                     160
1598
1599   Cys Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly
1600                   165                     170                     175
1601
1602   Lys Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu
1603               180                     185                     190
1604
1605   Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys
1606           195                     200                     205
1607
1608   Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys Arg Leu
1609           210                     215                     220
1610
1611   Asp Gly Ser Val Asp Phe Lys Lys Asn Trp Ile Gln Tyr Lys Glu Gly
1612   225                     230                     235                     240
1613
1614   Phe Gly His Leu Ser Pro Thr Gly Thr Thr Glu Phe Trp Leu Gly Asn
1615                   245                     250                     255
1616
1617   Glu Lys Ile His Leu Ile Ser Thr Gln Ser Ala Ile Pro Tyr Ala Leu
1618               260                     265                     270
1619
1620   Arg Val Glu Leu Glu Asp Trp Asn Gly Arg Thr Ser Thr Ala Asp Tyr
1621           275                     280                     285
1622
1623   Ala Met Phe Lys Val Gly Pro Glu Ala Asp Lys Tyr Arg Leu Thr Tyr
1624           290                     295                     300
1625
1626   Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp Ala Phe Asp Gly Phe Asp
1627   305                     310                     315                     320
1628
1629   Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe Thr Ser His Asn Gly Met
1630                   325                     330                     335
1631
1632   Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp Lys Phe Glu Gly Asn Cys
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1633                340                345                350
1634
1635   Ala Glu Gln Asp Gly Ser Gly Trp Trp Met Asn Lys Cys His Ala Gly
1636        355                360                365
1637
1638   His Leu Asn Gly Val Tyr Tyr Gln Gly Gly Thr Tyr Ser Lys Ala Ser
1639        370                375                380
1640
1641   Thr Pro Asn Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr
1642   385                390                395                400
1643
1644   Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn
1645                405                410                415
1646
1647   Arg Leu Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly Ala Lys
1648            420                425                430
1649
1650   Gln Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr
1651        435                440                445
1652
1653   Pro Glu Asp Asp Leu
1654        450
1655
1656   (2) INFORMATION FOR SEQ ID NO:7:
1657
1658        (i)  SEQUENCE CHARACTERISTICS:
1659             (A)  LENGTH: 10807 base pairs
1660             (B)  TYPE: nucleic acid
1661             (C)  STRANDEDNESS: double
1662             (D)  TOPOLOGY: linear
1663
1664
1665       (vii) IMMEDIATE SOURCE:
1666             (B)  CLONE: ovine beta-lactoglobulin
1667
1668
1669       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
1670
1671   ACGCGTGTCG ACCTGCAGGT CAACGGATCT CTGTGTCTGT TTTCATGTTA GTACCACACT        60
1672
1673   GTTTTGGTGG CTGTAGCTTT CAGCTACAGT CTGAAGTCAT AAAGCCTGGT ACCTCCAGCT       120
1674
1675   CTGTTCTCTC TCAAGATTGT GTTCTGCTGT TTGGGTCTTT AGTGTCTCCA CACAATTTTT       180
1676
1677   AGAATTGTTT GTTCTAGTTC TGTGAAAAAT GATGCTGGTA TTTTGATAAG GATTGCATTG       240
1678
1679   AATCTGTAAA GCTACAGATA TAGTCATTGG GTAGTACAGT CACTTTAACA ATATTAACTC       300
1680
1681   TTCACATCTG TGAGCATGAT ATATTTTCCC CCTCTATATC ATCTTCAATT CCTCCTATCA       360
1682
1683   GTTTCTTTCA TTGCAGTTTT CTGAGTACAG GTCTTACACC TCCTTGGTTA GAGTCATTCC       420
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INPUT SET: S1765.raw

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1687   GATAGCTCAT TGTTAGTGTA TATATAGAAA AGCAACAGAT TTCTATGTAT TAATTTTGTA    540
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1689   TCCTGCAACA GATTTCTATG TATTAATTTT GTATCCTGCT ACTTTACGGA ATTCACTTAT    600
1690
1691   TAGCTTTTTG GTGACATCTT GAGGATTTTC TGAAGAAAAT GGCATGGTAT GGTAGGACAA    660
1692
1693   GGTGTCATGT CATCTGCAAA CAGTGGCAGT TTTCCTTCTT CCCTTCCAAC CTGGATTTCT    720
1694
1695   TTGATTTCTT TCTGTCTGAG TACGACTAGG ATTCCCAATA CTATACCGAA TAAAAGTGGC    780
1696
1697   AAGAGTGGAC ATCCTTGTCT TATTTTTCTG ACCTTAGAGG AAATGCTTTC AGTTTTTCAC    840
1698
1699   CATTAATTAT AATGTTTACT GTGGGCTTGT CATATGTGGC CTTCATTATA TGGAGGTCTA    900
1700
1701   TTCCCTCTAT ACCCACCTTG TTGAGAGTTT TTATCATAAA AGTATGTTGA ATTTTGTCAA    960
1702
1703   AAGTTTTTCC TGCATCTATT GAGATGATTT TTACTCTTCA ATTCATTAAT GATTTTTATT   1020
1704
1705   CTTCATTTTG TTAATGATTT CCATTCTTCA ATTTGTTAAC GTGGTATATC ACATTGATTG   1080
1706
1707   ATTTGTGGAT ACCTTTGTAT CCCTGGGATA AACCTCACTT GATCATGAGC TTTCAATGTA   1140
1708
1709   TTTTTGAATT CACTTTGCTA ATATTCTGTT GGGTATTTTT GCATCTCTAT TCATCAATGA   1200
1710
1711   TATTGGCCTA AGAAAGGTTT TGTCTGGTTT TAGTATCAGG GTGATGCTGG CCTCATAGAG   1260
1712
1713   AGAGTTTAGA AGCATTTCCT CCTCTTTGAT TTTTCGGAAT AGTTTGAGTA GGATAGGTAT   1320
1714
1715   TAACTCTTCT TTAAATGTTT GGGGACTTCC CTGGTGAGCC GGTGGTTGAG AATCCGCCTC   1380
1716
1717   AGGGATGTGG GTTTGATCCC TGGTCAGGGA ACCATTAATA AGATCCCACA TGCTGCAGGC   1440
1718
1719   AACAAGCCCC CAAGCTGCAA CCACTGAGCT GCAACCGCTG CAGTGCCCAC AGGCCACGAC   1500
1720
1721   CAGAGAAAGC CCACATACAG CAGGGAAGAC CCAGCACAAC CGGAAAAAGG AGTTTGGTGG   1560
1722
1723   AATACAGCTG TGAAGCCGTC TGGTCCTGGA CTCCTGCTTG AGGGAATTTT TTAAAAATTA   1620
1724
1725   TTGATTCAAT TTCATTACTG GTAACTGGTC TGTTCATATT TTCTATTTCT TCCGGGTTCA   1680
1726
1727   GTCTTGGGAG ATTGTACATG CCTAGGAATG TGTCCGTTTC TTCTAGGTTG TCCATTTTAT   1740
1728
1729   TGGACATGCA TGGGAGCACA CAGCACCGAC CAGCGAGACT CATGCTGGCT TCCTGGGGCC   1800
1730
1731   AGGCTGGGGC CCCAAGCAGC ATGGCATCCT AGAGTGTGTG AAAGCCCACT GACCCTGCCC   1860
1732
1733   AGCCCCACAA TTTCATTCTG AGAAGTGATT CCTTGCTTCT GCACTTACAG GCCCAGGATC   1920
1734
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INPUT SET: S1765.raw

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1738
1739    TCTCCCTCCT ACAGTGGTCA GTCCCAGCTG CCCCAGGCCA GAGCTGCTTT ATTTCCGTCT    2100
1740
1741    CTCTCTCTGG ATGGTATTCT CTGGAAGCTG AAGGTTCCTG AAGTTATGAA TAGCTTTGCC    2160
1742
1743    CTGAAGGGCA TGGTTTGTGG TCACGGTTCA CAGGAACTTG GGAGACCCTG CAGCTCAGAC    2220
1744
1745    GTCCCGAGAT TGGTGGCACC CAGATTTCCT AAGCTCGCTG GGGAACAGGG CGCTTGTTTC    2280
1746
1747    TCCCTGGCTG ACCTCCCTCC TCCCTGCATC ACCCAGTTCT GAAAGCAGAG CGGTGCTGGG    2340
1748
1749    GTCACAGCCT CTCGCATCTA ACGCCGGTGT CCAAACCACC CGTGCTGGTG TTCGGGGGGC    2400
1750
1751    TACCTATGGG GAAGGGCTTC TCACTGCAGT GGTGCCCCCC GTCCCCTCTG AGATCAGAAG    2460
1752
1753    TCCCAGTCCG GACGTCAAAC AGGCCGAGCT CCCTCCAGAG GCTCCAGGGA GGGATCCTTG    2520
1754
1755    CCCCCCCGCT GCTGCCTCCA GCTCCTGGTG CCGCACCCTT GAGCCTGATC TTGTAGACGC    2580
1756
1757    CTCAGTCTAG TCTCTGCCTC CGTGTTCACA CGCCTTCTCC CCATGTCCCC TCCGTGTCCC    2640
1758
1759    CGTTTTCTCT CACAAGGACA CCGGACATTA GATTAGCCCC TGTTCCAGCC TCACCTGAAC    2700
1760
1761    AGCTCACATC TGTAAAGACC TAGATTCCAA ACAAGATTCC AACCTGAAGT TCCCGGTGGA    2760
1762
1763    TGTGAGTTCT GGGGCGACAT CCTTCAACCC CATCACAGCT TGCAGTTCAT CGCAAAACAT    2820
1764
1765    GGAACCTGGG GTTTATCGTA AAACCCAGGT TCTTCATGAA ACACTGAGCT TCGAGGCTTG    2880
1766
1767    TTGCAAGAAT TAAAGGTGCT AATACAGATC AGGGCAAGGA CTGAAGCTGG CTAAGCCTCC    2940
1768
1769    TCTTTCCATC ACAGGAAAGG GGGGCCTGGG GGCGGCTGGA GGTCTGCTCC CGTGAGTGAG    3000
1770
1771    CTCTTTCCTG CTACAGTCAC CAACAGTCTC TCTGGGAAGG AAACCAGAGG CCAGAGAGCA    3060
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1773    AGCCGGAGCT AGTTTAGGAG ACCCCTGAAC CTCCACCCAA GATGCTGACC AGCCAGCGGG    3120
1774
1775    CCCCCTGGAA AGACCCTACA GTTCAGGGGG GAAGAGGGGC TGACCCGCCA GGTCCCTGCT    3180
1776
1777    ATCAGGAGAC ATCCCCGCTA TCAGGAGATT CCCCCACCTT GCTCCCGTTC CCCTATCCCA    3240
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1779    ATACGCCCAC CCCACCCCTG TGATGAGCAG TTTAGTCACT TAGAATGTCA ACTGAAGGCT    3300
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1781    TTTGCATCCC CTTTGCCAGA GGCACAAGGC ACCCACAGCC TGCTGGGTAC CGACGCCCAT    3360
1782
1783    GTGGATTCAG CCAGGAGGCC TGTCCTGCAC CCTCCCTGCT CGGGCCCCCT CTGTGCTCAG    3420
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1785    CAACACACCC AGCACCAGCA TTCCCGCTGC TCCTGAGGTC TGCAGGCAGC TCGCTGTAGC    3480
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1787  CTGAGCGGTG TGGAGGGAAG TGTCCTGGGA GATTTAAAAT GTGAGAGGCG GGAGGTGGGA    3540
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1789  GGTTGGGCCC TGTGGGCCTG CCCATCCCAC GTGCCTGCAT TAGCCCCAGT GCTGCTCAGC    3600
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1791  CGTGCCCCCG CCGCAGGGGT CAGGTCACTT TCCCGTCCTG GGGTTATTAT GACTCTTGTC    3660
1792
1793  ATTGCCATTG CCATTTTTGC TACCCTAACT GGGCAGCAGG TGCTTGCAGA GCCCTCGATA    3720
1794
1795  CCGACCAGGT CCTCCCTCGG AGCTCGACCT GAACCCCATG TCACCCTTGC CCCAGCCTGC    3780
1796
1797  AGAGGGTGGG TGACTGCAGA GATCCCTTCA CCCAAGGCCA CGGTCACATG GTTTGGAGGA    3840
1798
1799  GCTGGTGCCC AAGGCAGAGG CCACCCTCCA GGACACACCT GTCCCCAGTG CTGGCTCTGA    3900
1800
1801  CCTGTCCTTG TCTAAGAGGC TGACCCCGGA AGTGTTCCTG GCACTGGCAG CCAGCCTGGA    3960
1802
1803  CCCAGAGTCC AGACACCCAC CTGTGCCCCC GCTTCTGGGG TCTACCAGGA ACCGTCTAGG    4020
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1805  CCCAGAGGGG ACTTCCTGCT TGGCCTTGGA TGGAAGAAGG CCTCCTATTG TCCTCGTAGA    4080
1806
1807  GGAAGCCACC CCGGGGCCTG AGGATGAGCC AAGTGGGATT CCGGGAACCG CGTGGCTGGG    4140
1808
1809  GGCCCAGCCC GGGCTGGCTG GCCTGCATGC CTCCTGTATA AGGCCCCAAG CCTGCTGTCT    4200
1810
1811  CAGCCCTCCA CTCCCTGCAG AGCTCAGAAG CACGACCCCA GGGATATCCC TGCAGCCATG    4260
1812
1813  AAGTGCCTCC TGCTTGCCCT GGGCCTGGCC CTCGCCTGTG GCGTCCAGGC CATCATCGTC    4320
1814
1815  ACCCAGACCA TGAAAGGCCT GGACATCCAG AAGGTTCGAG GGTTGGCCGG GTGGGTGAGT    4380
1816
1817  TGCAGGGCGG GCAGGGGAGC TGGGCCTCAG AGAGCCAAGA GAGGCTGTGA CGTTGGGTTC    4440
1818
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1820
1821  ACTGTCTTGC ATTCTGGAGG CTGGAAGCCC AAGATCCAGG TGTTGGCAGG GCTGGCTTCT    4560
1822
1823  CCTGCGGCCG CTCTCTGGGG AGCAGACGGC CGTCTTCTCC AGTCCTCTGC GCGCCCTGAT    4620
1824
1825  TTCCTCTTCC TGTGAGGCCA CCAGGCCTGC TGGAAACACG CCTGCCTGCG CAGCTTCACA    4680
1826
1827  CGACCTTTGT CATCTCTTTA AAGGCCATGT CTCCAGAGTC ATGTGTTGAA GTTCTGGGGG    4740
1828
1829  TTAGTGGGAC ACAGTTCAGC CCCTAAAAGA GTCTCTCTGC CCCTCAAATT TTCCCCACCT    4800
1830
1831  CCAGCCATGT CTCCCCAAGA TCCAAATGTT GCTACATGTG GGGGGGCTCA TCTGGGTCCC    4860
1832
1833  TCTTTGGGTT CAGTGTGAGT CTGGGGAGAG CATTCCCCAG GGTGCAGAGT TGGGGGGAGT    4920
1834
1835  ATCTCAGGGC TGCCCAGGCC GGGGTGGGAC AGAGAGCCCA CTGTGGGGCT GGGGGCCCCT    4980
1836
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INPUT SET: S1765.raw

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1837   TCCCACCCCC AGAGTGCAAC TCAAGGTCCC TCTCCAGGTG GCGGGGACTT GGCACTCCTT   5040
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1840
1841   CGTGGAGGAG CTGAAGCCCA CCCCCGAGGG CAACCTGGAG ATCCTGCTGC AGAAATGGTG   5160
1842
1843   GGCGTCTCTC CCCAACATGG AACCCCCACT CCCCAGGGCT GTGGACCCCC CGGGGGGTGG   5220
1844
1845   GGTGCAGGAG GGACCAGGGC CCCAGGGCTG GGGAAGAGGG CTCAGAGTTT ACTGGTACCC   5280
1846
1847   GGCGCTCCAC CCAAGGCTGC CCACCCAGGG CTTTTTTTTT TTTAAACTT TTATTAATTT   5340
1848
1849   GATGCTTCAG AACATCATCA AACAAATGAA CATAAACAT TCATTTTTGT TTACTTGGAA   5400
1850
1851   GGGGAGATAA AATCCTCTGA AGTGGAAATG CATAGCAAAG ATACATACAA TGAGGCAGGT   5460
1852
1853   ATTCTGAATT CCCTGTTAGT CTGAGGATTA CAAGTGTATT TGAGCAACAG AGAGACATTT   5520
1854
1855   TCATCATTTC TAGTCTGAAC ACCTCAGTAT CTAAAATGAA CAAGAAGTCC TGGAAACGAA   5580
1856
1857   GCAGTGTGGG GATAGGCCCG TGTGAAGGCT GCTGGGAGGC AGCAGACCTG GGTCTTCGGG   5640
1858
1859   CTCAAGCAGT TCCCGCTACC AGCCCTGTCC ACCTCAGACG GGGGTCAGGG TGCAGGAGAG   5700
1860
1861   AGCTGGATGG GTGTGGGGGC AGAGATGGGG ACCTGAACCC CAGGGCTGCC TTTTGGGGGT   5760
1862
1863   GCCTGTGGTC AAGGCTCTCC CTGACCTTTT CTCTCTGGCT TCATCTGACT TCTCCTGGCC   5820
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1865   CATCCACCCG GTCCCCTGTG GCCTGAGGTG ACAGTGAGTG CGCCGAGGCT AGTTGGCCAG   5880
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1873   TGTTCAAGAT CGATGGTGAG TCCGGGTCCC TGGGGACAC CCACCACCCC CGCCCCCGGG   6120
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1879   GGGGCGGTGG CCATGGGCAG GTCCCGGCTG GCGGGCTAAC CACCAGGGT GACACCCGAG   6300
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1923   TGAATCTAAC AGCCTTTGTT ACCGGGGAGT TTCAATTATT TCCCAAAATA AGAACTCAGG   7620
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1925   TACAAAGCCA TCTTTCAACT ATCACATCCT GAAAACAAAT GGCAGGTGAC ATTTTCTGTG   7680
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1927   CCGTAGCAGT CCCACTGGGC ATTTTCAGGG CCCCTGTGCC AGGGGGGCGC GGGCATCGGC   7740
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1933   GGGAGGGGAA CTAGGCCAAG GGGGAAGGGC AGGTGCTCTG GAGGGCAAGG GCAGACCTGC   7920
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1935   AGACCACCCT GGGGAGCAGG GACTGACCCC CGTCCCTGCC CCATAGTCAG GACCCCGGAG   7980
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1937   GTGGACAACG AGGCCCTGGA GAAATTCGAC AAAGCCCTCA AGGCCCTGCC CATGCACATC   8040
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RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/206,176

DATE: 03/23/94
TIME: 12:17:20

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1943    CTCCCAGGAG GAAGGGGTGG GGTGCAGCAC CCCGTGGGGG CCCCCTCCCC ACCCCCTGCC    8220
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1957    GGGAGGCTAG CGGTCCTTCT CCCGAGGAGG GGCTGTCCTG GAACCACCAG CCATGGAGAG    8640
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1959    GCTGGCAAGG GTCTGGCAGG TGCCCCAGGA ATCACAGGGG GGCCCCATGT CCATTTCAGG    8700
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1961    GCCCGGGAGC CTTGGACTCC TCTGGGGACA GACGACGTCA CCACCGCCCC CCCCCCATCA    8760
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1985    CTGATGTGAA GAGCTGACTC ATTTGAAAAG ACCCTGATGC TGGGAAAGAT TGAGGGCAGG    9480
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1987    AGGAGAAGGG GACGACAGAG GATGAGATGG TTGGATGGCA TCACCAACAC AATGGACATG    9540
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2013   TGAGTCACCA GACACTCGGG GGTGGCCCCG CCTTCAGGGT GCTCACAGTC TTCCCATCGT   10320
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2017   AGGTTCACCA GAGCTGAGCT GTCCTTTTGA ACCTAAAGAC ACACAGCTCT CGAAGGTTTT   10440
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2019   CTCTTTAATC TGGATTTAAG GCCTACTTGC CCCTCAAGAG GGAAGACAGT CCTGCATGTC   10500
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2021
2022   CCCAGGACAG CCACTCGGTG GCATCCGAGG CCACTTAGTA TTATCTGACC GCACCCTGGA   10560
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2024   ATTAATCGGT CCAAACTGGA CAAAAACCTT GGTGGGAAGT TTCATCCCAG AGGCCTCAAC   10620
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2026   CATCCTGCTT TGACCACCCT GCATCTTTTT TTCTTTTATG TGTATGCATG TATATATATA   10680
2027
2028   TATATATTTT TTTTTTTTTC ATTTTTTGGC TGTGCTGGCT GTTCGTTGCA GTTCGGTGCG   10740
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2030   CAGGCTTCTC TCTAGTTTCT CTCTAGTCTT CTCTTATCAC AGAGCAGTCT CTAGACGATC   10800
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2032   GACGCGT                                                            10807
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2034   (2) INFORMATION FOR SEQ ID NO:8:
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2036        (i) SEQUENCE CHARACTERISTICS:
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2038             (B) TYPE: nucleic acid
2039             (C) STRANDEDNESS: single
2040             (D) TOPOLOGY: linear
```

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2042
2043
2044        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
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2046   AATTCCGATC GACGCGTCGA CGATATACTC TAGACGATCG ACGCGTA                          47
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2050        (i) SEQUENCE CHARACTERISTICS:
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2052            (B) TYPE: nucleic acid
2053            (C) STRANDEDNESS: single
2054            (D) TOPOLOGY: linear
2055
2056
2057       (vii) IMMEDIATE SOURCE:
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2060
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2063   TGGATCCCCT GCCGGTGCCT CTGG                                                   24
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2066   (2) INFORMATION FOR SEQ ID NO:10:
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2068        (i) SEQUENCE CHARACTERISTICS:
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2070            (B) TYPE: nucleic acid
2071            (C) STRANDEDNESS: single
2072            (D) TOPOLOGY: linear
2073
2074
2075       (vii) IMMEDIATE SOURCE:
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2077
2078
2079        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
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2081   AACGCGTCAT CCTCTGTGAG CCAG                                                   24
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2085        (i) SEQUENCE CHARACTERISTICS:
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2089            (D) TOPOLOGY: linear
2090
2091
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2096         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:11:
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2098   ACTACGTAGT                                                           10
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2105               (C)  STRANDEDNESS: single
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2109        (vii)  IMMEDIATE SOURCE:
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2113         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:12:
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2115   CGACGCGGAT CCTACGTACC TGCAGCCATG TTTTCCATGA GG                      42
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2117   (2)  INFORMATION FOR SEQ ID NO:13:
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2119         (i)  SEQUENCE CHARACTERISTICS:
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2121               (B)  TYPE: nucleic acid
2122               (C)  STRANDEDNESS: single
2123               (D)  TOPOLOGY: linear
2124
2125
2126        (vii)  IMMEDIATE SOURCE:
2127               (B)  CLONE: ZC6627
2128
2129
2130         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:13:
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2132   AGGGCTTCGG CAAGCTTCAG G                                             21
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2134   (2)  INFORMATION FOR SEQ ID NO:14:
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2136         (i)  SEQUENCE CHARACTERISTICS:
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2139               (C)  STRANDEDNESS: single
2140               (D)  TOPOLOGY: linear
2141
2142
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2147        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:14:
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2149   GCCAAAGACT TACTTCCCTC TAGA                                          24
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2154        (i)  SEQUENCE CHARACTERISTICS:
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2157             (C) STRANDEDNESS: single
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2164
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2167   GCATGAACGT CGCGTGGTGG TTGTGCTACC                                    30
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2169   (2) INFORMATION FOR SEQ ID NO:16:
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2171        (i)  SEQUENCE CHARACTERISTICS:
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2173             (B) TYPE: nucleic acid
2174             (C) STRANDEDNESS: single
2175             (D) TOPOLOGY: linear
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2177
2178        (vii)  IMMEDIATE SOURCE:
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2182        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:16:
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2184   ACCACGCGAC GTTCATGCTC TAAAACCGTT                                    30
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2188        (i)  SEQUENCE CHARACTERISTICS:
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2205      (i) SEQUENCE CHARACTERISTICS:
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2208            (C) STRANDEDNESS: single
2209            (D) TOPOLOGY: linear
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2220 (2) INFORMATION FOR SEQ ID NO:19:
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2222      (i) SEQUENCE CHARACTERISTICS:
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2225            (C) STRANDEDNESS: single
2226            (D) TOPOLOGY: linear
2227
2228
2229      (vii) IMMEDIATE SOURCE:
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2232
2233      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
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2235 CGACGCGAAT CTACGTACC TGCAGCCATG AAACATCTAT TATTG           45
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2238 (2) INFORMATION FOR SEQ ID NO:20:
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2242            (B) TYPE: nucleic acid
2243            (C) STRANDEDNESS: single
2244            (D) TOPOLOGY: linear
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PATENT APPLICATION *US/08/206,176*

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2251          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:20:
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2253   GTGAGATTTT CAGATCTTGT C                                         21
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2257          (i)  SEQUENCE CHARACTERISTICS:
2258                     (A)  LENGTH: 21 base pairs
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2264          (vii)  IMMEDIATE SOURCE:
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2268          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:21:
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2270   AAGAATTACT GTGGCCTACC A                                         21
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2272   (2)  INFORMATION FOR SEQ ID NO:22:
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2274          (i)  SEQUENCE CHARACTERISTICS:
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2277                     (C)  STRANDEDNESS: single
2278                     (D)  TOPOLOGY: linear
2279
2280
2281
2282          (vii)  IMMEDIATE SOURCE:
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2285
2286          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:22:
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2288   GCTGCGGAAT CTACGTACT ATTGCTGTGG GAA                            33
2289
2290   (2)  INFORMATION FOR SEQ ID NO:23:
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2292          (i)  SEQUENCE CHARACTERISTICS:
2293                     (A)  LENGTH: 45 base pairs
2294                     (B)  TYPE: nucleic acid
2295                     (C)  STRANDEDNESS: single
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DATE: 03/23/94
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INPUT SET: S1765.raw

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2296              (D) TOPOLOGY: linear
2297
2298
2299      (vii) IMMEDIATE SOURCE:
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2301
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2303      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
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2305  CGACGCGGAT CCTACGTACC TGCAGCCATG AGTTGGTCCT TGCAC              45
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2307  (2) INFORMATION FOR SEQ ID NO:24:
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2309      (i) SEQUENCE CHARACTERISTICS:
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2311              (B) TYPE: nucleic acid
2312              (C) STRANDEDNESS: single
2313              (D) TOPOLOGY: linear
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2315
2316      (vii) IMMEDIATE SOURCE:
2317              (B) CLONE: zc6517
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2319
2320      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
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2322  GTCTCTGGTA GCAACATACT A                                      21
2323
2324
2325  (2) INFORMATION FOR SEQ ID NO:25:
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2327      (i) SEQUENCE CHARACTERISTICS:
2328              (A) LENGTH: 22 base pairs
2329              (B) TYPE: nucleic acid
2330              (C) STRANDEDNESS: single
2331              (D) TOPOLOGY: linear
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2333
2334      (vii) IMMEDIATE SOURCE:
2335              (B) CLONE: zc6516
2336
2337
2338      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
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2341
2342  (2) INFORMATION FOR SEQ ID NO:26:
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2344      (i) SEQUENCE CHARACTERISTICS:
2345              (A) LENGTH: 22 base pairs
2346              (B) TYPE: nucleic acid
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2347              (C)  STRANDEDNESS: single
2348              (D)  TOPOLOGY: linear
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2351      (vii)  IMMEDIATE SOURCE:
2352              (B)  CLONE: zc6515
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2354
2355       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:26:
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2357  GGGTTTCTAG CCCTACTAGT AG                                          22
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2359
2360  (2)  INFORMATION FOR SEQ ID NO:27:
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2362       (i)  SEQUENCE CHARACTERISTICS:
2363              (A)  LENGTH: 47 base pairs
2364              (B)  TYPE: nucleic acid
2365              (C)  STRANDEDNESS: single
2366              (D)  TOPOLOGY: linear
2367
2368
2369
2370       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:27:
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2372  AAGCTACGCG TCGATCGTCT AGAGTATATC GTCGACGCGT CGATCGG
2373
2374
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47

↑
Insert

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/206,176*

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/206,176*

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APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/08/206,176*

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Line	Original Text	Corrected Text